



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 163003

TO: Sean McGarry
Art Unit: 1635
Location: rem/2d19/2c18
Serial Number: 09/927046

Tuesday, May 17, 2005

From: Beverly Shears
Location: Biotech-Chem Library
REM 1A54
Phone: 571-272-2528
beverly.shears@uspto.gov

Search Notes

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From: McGarry, Sean
Sent: Tuesday, May 10, 2005 10:18 AM
To: STIC-Biotech/ChemLib
Subject: SEQ SEARCH 09/927046

Sean McGarry
AU 1635
REM 02D19 Office
REM 2C18 Mailbox
X20761

Please a search of SEQ ID NOS: 143 and 2332 length limited (nt ≤ 100).

Thank You

seq 143 - 17NA
2332 - 38NA

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2- _____
Date Searcher Picked up: _____
Date Completed: _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA#: _____ AA#: _____
Interference: _____ SPDI: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure#: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIS: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

Date completed: _____

Searcher: Beverly e 2528

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Search Site

_____ STIC
_____ CM-1
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Type of Search

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09/927046

FILE 'REGISTRY' ENTERED AT 16:17:32 ON 16 MAY 2005

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CN GenBank AX580494 (9CI) (CA INDEX NAME)
CI MAN
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L2 ANSWER 3 OF 4 REGISTRY COPYRIGHT 2005 ACS on STN
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OTHER NAMES:

CN 332: PN: WO0211674 SEQID: 2332 claimed RNA

CI MAN

SQL 38

SEQ 1 ccugcaaucu gaugaggccg uuaggccgaa aaaucagg
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HITS AT: 1-38

REFERENCE 1: 136:194272

L2 ANSWER 4 OF 4 REGISTRY COPYRIGHT 2005 ACS on STN
RN 398240-93-2 REGISTRY
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CN 144: PN: WO0211674 SEQID: 143 claimed RNA

CI MAN

SQL 17

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REFERENCE 1: 136:194272

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L3 1 S L2

L3 ANSWER 1 OF 1 CAPLUS COPYRIGHT 2005 ACS on STN
ED Entered STN: 15 Feb 2002
ACCESSION NUMBER: 2002:122738 CAPLUS

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09/927046

DOCUMENT NUMBER: 136:194272
 TITLE: Ribozymes and antisense oligonucleotides for the inhibition of gene expression by calcium-activated chloride channel-1 gene CLCA-1
 INVENTOR(S): Thompson, James; McSwiggen, James; McKenzie, Timothy; Ayers, David; Szymkowski, David E.; Grupe, Andrew
 PATENT ASSIGNEE(S): Ribozyme Pharmaceuticals, Incorporated, USA; Syntex (U.S.A.) LLC
 SOURCE: PCT Int. Appl., 152 pp.
 CODEN: PIXXD2
 DOCUMENT TYPE: Patent
 LANGUAGE: English
 FAMILY ACC. NUM. COUNT: 1
 PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002011674	A2	20020214	WO 2001-US24970	20010809
WO 2002011674	A3	20030925		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG US 2003064946 A1 20030403 US 2001-927046 20010809 PRIORITY APPLN. INFO.: US 2000-224383P P 20000809				

AB Nucleic acid mols., including antisense and enzymic nucleic acid mols., such as hammerhead ribozymes, DNazymes, and GeneBlocs, which modulate the expression of calcium-activated chloride channels (CLCA1, CLCA2, CLCA3, and CLCA4) are provided. A target discovery target validation approach was used for finding genes that are involved in chronic mucous hypersecretion. The reporter system consists of a plasmid construct, termed pMUC5AC-EGFP, bearing a gene coding for green fluorescent protein (GFP). The promoter region of the GFP gene is replaced by a portion of the mucin 5AC promoter sufficient to direct efficient transcription of the GFP gene; the plasmid also contains the neomycin drug resistance gene. The cell line selected as host for these studies, NCI-H292 (ATCC CRL-1848), is derived from a human lung mucoepidermoid carcinoma. A ribozyme library with two randomized regions comprising six-nucleotide binding "arms" is used to enrich cells for non-responders to mucin induction and a bioinformatics approach used to identify human CLCA1 as a regulator of MUC5AC expression. Antisense, hammerhead, DNzyme, NCH, amberzyme, zinzyme, and G-Cleaver ribosome binding/cleavage sites in CLCA1 were identified. The nucleic acid mols. are individually analyzed by computer folding to assess whether the sequences fold into the appropriate secondary structure and to anneal to various sites in the RNA target. Those nucleic acid mols. with unfavorable intramol. interactions such as between the binding arms and the catalytic core are eliminated from consideration. Varying binding arm lengths can be chosen to optimize activity.

IT 398240-93-2

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09/927046

RL: BSU (Biological study, unclassified); PRP (Properties); BIOL
(Biological study)
(CLCA-1 gene target region for hammerhead ribozyme; ribozymes and
antisense oligonucleotides for the inhibition of gene expression by
calcium-activated chloride channel-1 gene CLCA-1)

IT 399091-50-0

RL: PRP (Properties); THU (Therapeutic use); BIOL (Biological study);
USES (Uses)
(hammerhead ribozyme; ribozymes and antisense oligonucleotides for
the inhibition of gene expression by calcium-activated chloride
channel-1 gene CLCA-1)

(FILE 'MEDLINE, BIOSIS, EMBASE' ENTERED AT 16:21:55 ON 16 MAY 2005)

L4 0 S L2

FILE 'HOME' ENTERED AT 16:22:05 ON 16 MAY 2005

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09/927046

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(FILE 'HOME' ENTERED AT 16:08:34 ON 16 MAY 2005)
DEL HIS Y

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MC Garry, S.
09/19/27046 Page 1
Seq. ID 143 & 2332GenCore version 5.1.6
Copyright (c) 1993 - 2005 Comugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 13, 2005, 16:49:04 ; Search time 488.055 Seconds
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1687.800 Million cell updates/sec

Title: US-09-927-046-143

Perfect score: 17

Sequence: 1 ccgaaunucagcag 17

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 2238514

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 100 summaries

Database :

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1: gb_da:*
2: gb_hcg:*
3: gb_in:*
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11: gb_scs:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	17	100.0	17	6	AX578305 Sequence
2	16	94.1	17	6	AX578304 Sequence
3	16	94.1	17	6	AX578867 Sequence
4	15	88.2	15	6	AX583575 Sequence
5	15	88.2	15	6	AX583576 Sequence
6	15	88.2	15	6	AX583577 Sequence
7	15	88.2	15	6	AX583578 Sequence
8	15	88.2	15	6	AX583579 Sequence
9	14	82.4	15	6	CO306794 Sequence
10	14	82.4	15	6	AX583574 Sequence
11	14	82.4	17	6	AX578306 Sequence
12	14	82.4	19	6	AX699218 Sequence
13	14	82.4	22	6	AX771264 Sequence
14	13	78.8	52	6	AX356812 Sequence
15	13	76.5	15	6	AX583578 Sequence
16	13	76.5	17	6	AX579409 Sequence
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ALIGNMENTS

RESULT 1
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LOCUS Sequence 143 from Patent WO0211674.
ACCESSION AX578305
VERSION AX578305.1 GI:27647507
KEYWORDS
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ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS 1
TITLE Thompson, J., Mcswigen, J., McKenzie, T., Ayers, D., Szymkowski, D.E.
and Grupe, A.
METHOD and reagent for the inhibition of calcium activated chloride
channel-1 (clca-1)
JOURNAL Patent: WO 0211674-A 143 14-FEB-2002;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;
Thompson, James (US)
LOCATION/Qualifiers

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RESULT 2
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LOCUS Sequence 142 from Patent WO0211674.
ACCESSION AX578304
VERSION AX578304.1 GI:27647506
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ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE
AUTHORS 1
TITLE Thompson, J., Mcswigen, J., McKenzie, T., Ayers, D., Szymkowski, D.E.
and Grupe, A.
METHOD and reagent for the inhibition of calcium activated chloride
channel-1 (clca-1)
JOURNAL Patent: WO 0211674-A 142 14-FEB-2002;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;
Thompson, James (US)
LOCATION/Qualifiers

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ACCESSION AX578867
VERSION AX578867.1 GI:27648069
KEYWORDS
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ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS 1
TITLE Thompson, J., Mcswigen, J., McKenzie, T., Ayers, D., Szymkowski, D.E.
and Grupe, A.
METHOD and reagent for the inhibition of calcium activated chloride
channel-1 (clca-1)
JOURNAL Patent: WO 0211674-A 705 14-FEB-2002;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;
Thompson, James (US)
LOCATION/Qualifiers

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LOCUS Sequence 5413 from Patent WO0211674.
ACCESSION AX583575
VERSION AX583575.1 GI:27655385
KEYWORDS
SOURCE
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE
AUTHORS 1
TITLE Thompson, J., Mcswigen, J., McKenzie, T., Ayers, D., Szymkowski, D.E.
and Grupe, A.
METHOD and reagent for the inhibition of calcium activated chloride
channel-1 (clca-1)
JOURNAL Patent: WO 0211674-A 5413 14-FEB-2002;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;
Thompson, James (US)
LOCATION/Qualifiers

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LOCUS Sequence 5414 from Patent WO0211674.
ACCESSION AX583576
VERSION AX583576.1 GI:27655386
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ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
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Qy 2 CUGAUUUCAGCAG 16
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RESULT 6
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LOCUS Sequence 5415 from Patent WO0211674.
ACCESSION AX583577
VERSION AX583577.1 GI:27655387
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ACCESSION AX578303
VERSION AX578303.1 GI:27647505
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ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES
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Db 3 CCTGATTCATTCGCA 17

RESULT 8
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ACCESSION CQ306794
VERSION CQ306794.1 GI:41267371
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DEFINITION Sequence 5412 from Patent WO0211674.
ACCESSION AX583574
VERSION AX583574.1 GI:27655384KEYWORDS
SOURCE
ORGANISM
synthetic construct
other sequences; artificial sequences.REFERENCE
AUTHORS1 Thompson, J., McSwiggen, J., McKenzie, T., Ayers, D., Szymkowski, D.E.
and Grube, A.
Method and reagent for the inhibition of calcium activated chloride
channel-1 (clca-1)
Patent: WO 0211674-A 5412 14-FEB-2002;JOURNAL
RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;
Thompson, James (US)FEATURES
source1..15
Location/Qualifiers

/organism="synthetic construct"

/mol_type="unassigned DNA"

/db_xref="taxon:32630"

/note="Enzymatic Nucleic Acid"

ORIGIN

Query Match 82.4%; Score 14; DB 6; Length 15;
Best Local Similarity 57.1%; Pred. No. 1.3e+04;
Matches 8; Conservative 6; Mismatches 0; Indels 0; Gaps 0;Qy 1 CCUGAUVUUCAGG 14
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Db 2 CCTGATTTCATTC 15RESULT 10
AX578306LOCUS AX578306 17 bp RNA linear PAT 10-JAN-2003
DEFINITION Sequence 144 from Patent WO0211674.
ACCESSION AX578306
VERSION AX578306.1 GI:27647508KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)1 Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.REFERENCE
AUTHORS1 Thompson, J., McSwiggen, J., McKenzie, T., Ayers, D., Szymkowski, D.E.
and Grube, A.
Method and reagent for the inhibition of calcium activated chloride
channel-1 (clca-1)
Patent: WO 0211674-A 144 14-FEB-2002;JOURNAL
RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;
Thompson, James (US)FEATURES
source1..17
Location/Qualifiers

/organism="Homo sapiens"

/mol_type="unassigned RNA"

/db_xref="taxon:9606"

ORIGIN

Query Match 82.4%; Score 14; DB 6; Length 17;
Best Local Similarity 64.3%; Pred. No. 1.3e+04;
Matches 9; Conservative 5; Mismatches 0; Indels 0; Gaps 0;Qy 4 GAUUCUUCAGG 17
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Db 1 GATTTCATTGCAG 14RESULT 11
AX699218/cLOCUS AX699218 19 bp DNA linear PAT 29-MAY-2003
DEFINITION Sequence 159 from Patent WO03000727.
ACCESSION AX699218
VERSION AX699218.1 GI:29499868KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
other sequences; artificial sequences.REFERENCE
AUTHORS1 Zhang, Y., Moffatt, M., Cookson, W. and Tinsley, J.O.
Atopy
Patent: WO 03000727-A 159 03-JAN-2003;JOURNAL
ISIS INNOVATION LIMITED (GB)FEATURES
source1..19
Location/Qualifiers

/organism="synthetic construct"

/mol_type="unassigned DNA"

/db_xref="taxon:32630"

/note="Primer"

ORIGIN

Query Match 82.4%; Score 14; DB 6; Length 19;
Best Local Similarity 64.3%; Pred. No. 1.3e+04;
Matches 9; Conservative 5; Mismatches 0; Indels 0; Gaps 0;Qy 4 GAUUCUUCAGG 17
|||||:|||||
Db 19 GATTTCATTGCAG 6RESULT 12
AX771264LOCUS AX771264 22 bp DNA linear PAT 02-JUL-2003
DEFINITION Sequence 12 from Patent WO03038079.
ACCESSION AX771264
VERSION AX771264.1 GI:32438307KEYWORDS
SOURCE
ORGANISM
synthetic construct
other sequences; artificial sequences.REFERENCE
AUTHORS1 Aerts, J.M. and Boot, R.G.
A mammalian mucinase, its recombinant production, and its use in
therapy or prophylaxis against diseases in which mucus is involved
or infectious diseases
Patent: WO 03038079-A 12 08-MAY-2003;JOURNAL
MacroDyme B.V. (NL)FEATURES
source1..22
Location/Qualifiers

/organism="synthetic construct"

/mol_type="unassigned DNA"

/db_xref="taxon:32630"

/note="Primer HAS3-A-tail"

ORIGIN

Query Match 78.8%; Score 13.4; DB 6; Length 22;
Best Local Similarity 53.3%; Pred. No. 2.8e+04;
Matches 8; Conservative 6; Mismatches 1; Indels 0; Gaps 0;Qy 2 CUGAUVUUCAGG 16
|||:|||||
Db 8 CTGATTTTATTGCAG 22RESULT 13
AX956812/cLOCUS AX956812 52 bp DNA linear PAT 08-JAN-2004
DEFINITION Sequence 17 from Patent EP1367120.
ACCESSION AX956812
VERSION AX956812.1 GI:40785287

KEYWORDS

SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE other sequences; artificial sequences.
AUTHORS 1 Takeshima, S., Sogabe, A. and Oka, M.
TITLE Modified pyrrolizidine quinone (PQQ) dependent glucose dehydrogenase with superior substrate specificity and stability
JOURNAL Patent: EP 1367120-A 17 03-DEC-2003;
TOYO BOSEKI KAKUSHIKI KAISHA (JP)
FEATURES Location/Qualifiers
source 1..52
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
misc_feature 18..26
/note="page 43, line 2 from the bottom"

ORIGIN
Query Match 78.8%; Score 13.4; DB 6; Length 52;
Best Local Similarity 53.3%; Pred. No. 2.7e+04;
Matches 8; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 3 AUAUUCAUUGCAGG 17
Db 15 TGATTGATTGCAGG 1
:::|||||
:::|||||

RESULT 14
AX583578 15 bp DNA linear PAT 10-JAN-2003
LOCUS Sequence 5416 from Patent WO0211674.
ACCESSION AX583578
VERSION AX583578.1 GI:27655388
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE other sequences; artificial sequences.
AUTHORS 1 Thompson, J., Mcswiggen, J., McKenzie, T., Ayers, D., Szymkowski, D.E.
TITLE and Grube, A.
METHOD and reagent for the inhibition of calcium activated chloride channel-1 (clca-1)
JOURNAL Patent: WO 0211674-A 5416 14-FEB-2002;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;
Thompson, James (US)
FEATURES Location/Qualifiers
source 1..15
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Enzymatic Nucleic Acid"

ORIGIN
Query Match 76.5%; Score 13; DB 6; Length 15;
Best Local Similarity 61.5%; Pred. No. 4.7e+04;
Matches 8; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AUUUCAUUGCAGG 17
Db 1 ATTTCATTGCAGG 13
||||:|||||
||||:|||||

RESULT 15
AX579409 17 bp RNA linear PAT 10-JAN-2003
LOCUS Sequence 1247 from Patent WO0211674.
ACCESSION AX579409
VERSION AX579409.1 GI:27648611
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 Thompson, J., Mcswiggen, J., McKenzie, T., Ayers, D., Szymkowski, D.E.
AUTHORS and Grube, A.
TITLE Method and reagent for the inhibition of calcium activated chloride channel-1 (clca-1)
JOURNAL Patent: WO 0211674-A 1247 14-FEB-2002;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;
Thompson, James (US)
FEATURES Location/Qualifiers
source 1..17
/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 76.5%; Score 13; DB 6; Length 17;
Best Local Similarity 61.5%; Pred. No. 4.7e+04;
Matches 8; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AUUUCAUUGCAGG 17
Db 1 ATTTCATTGCAGG 13
||||:|||||
||||:|||||

RESULT 16
AX579833 17 bp RNA linear PAT 10-JAN-2003
LOCUS Sequence 1671 from Patent WO0211674.
ACCESSION AX579833
VERSION AX579833.1 GI:27649035
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS 1 Thompson, J., Mcswiggen, J., McKenzie, T., Ayers, D., Szymkowski, D.E.
TITLE and Grube, A.
METHOD and reagent for the inhibition of calcium activated chloride channel-1 (clca-1)
JOURNAL Patent: WO 0211674-A 1671 14-FEB-2002;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;
Thompson, James (US)
FEATURES Location/Qualifiers
source 1..17
/organism="Homo sapiens"
/mol_type="unassigned RNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 76.5%; Score 13; DB 6; Length 17;
Best Local Similarity 53.8%; Pred. No. 4.7e+04;
Matches 7; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCUGAUUUCAGG 13
Db 5 CCTGATTTCATTG 17
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||||:|||||

RESULT 17
CQ549043 60 bp DNA linear PAT 30-JAN-2004
LOCUS Sequence 18678 from Patent WO0210449.
ACCESSION CQ549043
VERSION CQ549043.1 GI:41515470
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS 1 Shoshan, A., Wasserman, A., Mintz, E., Mintz, L. and Paigler, S.
TITLE Oligonucleotide library for detecting rna transcripts and splice

variants that populate a transcriptome
Patent: WO 0210449-A 18678 07-FEB-2002;
Compugen Inc. (US)
Location/Qualifiers
1. .60
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 76.5%; Score 13; DB 6; Length 60;
Best Local Similarity 61.5%; Pred. No. 4.5e+04;
Matches 8; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 4 GAUUUCAUUGCAG 16
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30 GATTTCATTGCAG 42

Db

RESULT 18
AX496844/c 67 bp DNA linear PAT 26-SEP-2002
LOCUS
DEFINITION Sequence 18 from Patent WO02059371.
ACCESSION AX496844
VERSION AX496844.1 GI:23342364
KEYWORDS
SOURCE
ORGANISM
synthetic construct
other sequences; artificial sequences.

REFERENCE
AUTHORS
1 Myrick, J., Ren, B., Robert, F., Simon, I. and Young, R. A.
TITLE Genome-wide location and function of dna binding proteins
JOURNAL Patent: WO 02059371-A 18 01-AUG-2002;
WHITEHEAD BIOMEDICAL INST (US)
Location/Qualifiers
1. .67
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="21373 SW16 18 myc backward primer"

ORIGIN

Query Match 76.5%; Score 13; DB 6; Length 67;
Best Local Similarity 53.8%; Pred. No. 4.4e+04;
Matches 7; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 3 UGAUUUCAUUGCA 15
:||||:|||||
43 TGATTTCATTGCA 31

Db

RESULT 19
CQ081942/c 80 bp DNA linear PAT 20-JAN-2004
LOCUS
DEFINITION Sequence 17742 from Patent WO0157278.
ACCESSION CQ081942
VERSION CQ081942.1 GI:41051811
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS
1 Penn, S. G., Hanzel, D. K., Chen, W. and Rank, D. R.
TITLE Human genome-derived single exon nucleic acid probes useful for
analysis of gene expression in human heLa cells or other human
JOURNAL cervical epithelial cells
Patent: WO 0157278-A 17742 09-AUG-2001;
Aeomica, Inc. (US)
Location/Qualifiers
1. .80
/organism="Homo sapiens"
/mol_type="unassigned DNA"

FEATURES
source

/db_xref="taxon:9606"
/note="MAP TO AC002472.3-EXPRESSED IN HELA, SIGNAL =
11-EST HUMAN HIT: BF311025.1, EVALUE 1.00e-37-NT HIT:
AB002059.1, EVALUE 6.00e-38"

ORIGIN

Query Match 75.3%; Score 12.8; DB 6; Length 80;
Best Local Similarity 56.2%; Pred. No. 5.7e+04;
Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 CUGAUUUCAGCAG 17
|:||||:|||||
57 CTGATTGCATTTCAGG 42

Db

RESULT 20
CQ116609/c 80 bp DNA linear PAT 21-JAN-2004
LOCUS
DEFINITION Sequence 25468 from Patent WO0157272.
ACCESSION CQ116609
VERSION CQ116609.1 GI:41086479
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS
1 Penn, S. G., Hanzel, D. K., Chen, W. and Rank, D. R.
TITLE Human genome-derived single exon nucleic acid probes useful for
analysis of gene expression in human placenta
JOURNAL Patent: WO 0157272-A 25468 09-AUG-2001;
Aeomica, Inc. (US)
Location/Qualifiers
1. .80
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="MAP TO AC002472.3-EXPRESSED IN PLACENTA, SIGNAL =
6.7-EST HUMAN HIT: BF311025.1, EVALUE 1.00e-37-NT HIT:
AB002059.1, EVALUE 6.00e-38"

ORIGIN

Query Match 75.3%; Score 12.8; DB 6; Length 80;
Best Local Similarity 56.2%; Pred. No. 5.7e+04;
Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 CUGAUUUCAGCAG 17
|:||||:|||||
57 CTGATTGCATTTCAGG 42

Db

RESULT 21
CQ155325/c 80 bp DNA linear PAT 21-JAN-2004
LOCUS
DEFINITION Sequence 25347 from Patent WO0157276.
ACCESSION CQ155325
VERSION CQ155325.1 GI:41162677
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS
1 Penn, S. G., Hanzel, D. K., Chen, W. and Rank, D. R.
TITLE Human genome-derived single exon nucleic acid probes useful for
analysis of gene expression in human bone marrow
JOURNAL Patent: WO 0157276-A 25347 09-AUG-2001;
Aeomica, Inc. (US)
Location/Qualifiers
1. .80
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

FEATURES
source

FEATURES
source
Location/Qualifiers
1.80
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="MAP TO AC002472.3-EXPRESSED IN LUNG, SIGNAL = 12-BEST_HUMAN HIT: BF311025.1, EVALUE 1.00e-37-NT HIT: AB02059.1, EVALUE 6.00e-38"

ORIGIN
Query Match 75.3%; Score 12.8; DB 6; Length 80;
Best Local Similarity 56.2%; Pred. No. 5.7e+04;
Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 2 CUGAUNUCAUUGCAGG 17
|||:|||||
57 CTGATTCATTTCAGG 42

RESULT 26
LOCUS CQ350689 80 bp DNA linear PAT 23-JAN-2004
DEFINITION Sequence 24783 from Patent WO0157275.
ACCESSION CQ350689
VERSION CQ350689.1 GI:41299760
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
TITLE Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human brain
JOURNAL Patent: WO 0157275-A 24783 09-AUG-2001;
Acemica, Inc. (US)
Location/Qualifiers
1.80
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="MAP TO AC002472.3-EXPRESSED IN BRAIN, SIGNAL = 13-BEST_HUMAN HIT: BF311025.1, EVALUE 1.00e-37-NT HIT: AB02059.1, EVALUE 6.00e-38"

ORIGIN
Query Match 75.3%; Score 12.8; DB 6; Length 80;
Best Local Similarity 56.2%; Pred. No. 5.7e+04;
Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 2 CUGAUNUCAUUGCAGG 17
|||:|||||
57 CTGATTCATTTCAGG 42

RESULT 27
LOCUS CR378747 86 bp DNA linear STS 24-MAR-2004
DEFINITION Arabidopsis thaliana transposon insertion STS GT_3.7348, sequence tagged site.
ACCESSION CR378747
VERSION CR378747.1 GI:45725203
KEYWORDS STS; STS, sequence tagged site.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eustosids II; Brassicales; Brassicaceae; Arabidopsids.

REFERENCE
AUTHORS Clarke, J.H., Bowles, B., Carter, J., Hart, D., McCullagh, B., Walsh, S., Langham, S., Legrys, C., Jones, J.D.G. and Bevan, M.
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 86)

AUTHORS Clarke, J.H.
TITLE Direct Submission
JOURNAL Submitted (22-MAR-2004) Clarke J.H., John Innes Centre, Colney lane, Norwich, NR4 7UJ, UK
COMMENT AT denotes an activation tag dissociation transposon within a single line, ET an enhancer trap dissociation transposon, GT a gene trap dissociation transposon, MT a mis-expression enhancer trap dissociation transposon, SM a defective suppressor mutator transposon. _3 denotes a sequence derived from the 3' end of the transposon, _5 denotes a sequence derived from the 5' end of the transposon BBSRC GARNER, ATIS project
On-line seed stock requests: <http://nasc.nott.ac.uk/> NASC stock code: N174684.

FEATURES
source
Location/Qualifiers
1.86
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/variety="landsberg erecta NASC stock code NW20"
/cultivar="D86 x Ac1"
/db_xref="taxon:3702"
/clone="AP001305"
1.86
/standard_name="GT_3.7348"

ORIGIN
Query Match 75.3%; Score 12.8; DB 11; Length 86;
Best Local Similarity 56.2%; Pred. No. 5.7e+04;
Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY 1 CUGAUNUCAUUGCAGG 16
|||:|||||
73 CCGGTTTCATTTCAGG 58

RESULT 28
LOCUS CQ001210 100 bp DNA linear PAT 16-JAN-2004
DEFINITION Sequence 12672 from Patent EP1260592.
ACCESSION CQ001210
VERSION CQ001210.1 GI:41007848
KEYWORDS
SOURCE Escherichia coli
ORGANISM Escherichia coli
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.

REFERENCE
1 Donner, H., Drescher, B., Huber, A. and Weber, J.
AUTHORS Biochip
TITLE Patent: EP 1260592-A 12672 27-NOV-2002;
JOURNAL MWG -Biotech AG (DE)
Location/Qualifiers
1.100
/organism="Escherichia coli"
/mol_type="unassigned DNA"
/db_xref="taxon:562"
/note="Y141 D4279 U00096 complement(449671__450999)"

ORIGIN
Query Match 75.3%; Score 12.8; DB 6; Length 100;
Best Local Similarity 62.5%; Pred. No. 5.7e+04;
Matches 10; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 2 CUGAUNUCAUUGCAGG 17
|||:|||||
11 CTGATTCATTTCAGG 26

RESULT 29
LOCUS AX998611 100 bp DNA linear PAT 16-JAN-2004
DEFINITION Sequence 10074 from Patent EP1260592.
ACCESSION AX998611
VERSION AX998611.1 GI:41004957

KEYWORDS
SOURCE Escherichia coli
ORGANISM Escherichia coli
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.

REFERENCE
1 Donner, H., Drescher, B., Huber, A. and Weber, J.
AUTHORS Blochid
TITLE Patent: EP 1260592-A 10074 27-NOV-2002;
JOURNAL MWG - Biotech AG (DE)
FEATURES Location/Qualifiers
source 1..100
/organism="Escherichia coli"
/mol_type="unassigned DNA"
/db_xref="taxon:562"
/note="Inta b2523 U00096 2754180_2755421"

ORIGIN
Query Match 75.3%; Score 12.8; DB 6; Length 100;
Best Local Similarity 56.2%; Pred. No. 5.7e+04;
Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCUGAUNUCATGCGAG 16
Db 82 CCTGATGTCATTGAG 97

RESULT 30
AR298188/c AR298188 20 bp DNA linear PAT 12-JUN-2003
LOCUS AR298188
DEFINITION Sequence 9923 from patent US 6537751.
ACCESSION AR298188
VERSION AR298188.1 GI:31685472
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
FEATURES Unclassified.
1 (bases 1 to 20)
AUTHORS Cohen, D., Chumakov, I. and Blumenfeld, M.
TITLE Biallelic markers for use in constructing a high density
disequilibrium map of the human genome
JOURNAL Patent: US 6537751-A 9923 25-MAR-2003;
FEATURES Location/Qualifiers
source 1..20
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 72.9%; Score 12.4; DB 6; Length 20;
Best Local Similarity 50.0%; Pred. No. 1e+05;
Matches 7; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCUGAUNUCATGCG 14
Db 20 CCTGATTTAATGCG 7

RESULT 31
CQ759952/c CQ759952 25 bp DNA linear PAT 03-MAR-2004
LOCUS CQ759952
DEFINITION Sequence 2 from Patent EP1382685.
ACCESSION CQ759952
VERSION CQ759952.1 GI:44903617
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.

REFERENCE
1 Rieping, M. and Siebelt, N.
AUTHORS Process for the fermentative preparation of L-amino acids using
TITLE strains of the enterobacteriaceae family with overexpressed rseB
JOURNAL gene
Patent: EP 1382685-A 2 21-JAN-2004;

FEATURES Degussa AG (DE)
source Location/Qualifiers
1..25
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match 72.9%; Score 12.4; DB 6; Length 25;
Best Local Similarity 57.1%; Pred. No. 1e+05;
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 3 UGAUUDUCATGCGAG 16
Db 21 TGATTTCACTGCGAG 8

RESULT 32
AX683923/c AX683923 25 bp DNA linear PAT 29-MAR-2003
LOCUS AX683923
DEFINITION Sequence 4 from Patent WO03008612.
ACCESSION AX683923
VERSION AX683923.1 GI:29370935
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
FEATURES other sequences; artificial sequences.

REFERENCE
1 Rieping, M.
AUTHORS Process for the preparation of L-amino acids using strains of the
TITLE Enterobacteriaceae family which contain an enhanced rseB or rseC
JOURNAL gene
Patent: WO 03008612-A 4 30-JAN-2003;
FEATURES Location/Qualifiers
source 1..25
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer rseC2"

ORIGIN
Query Match 72.9%; Score 12.4; DB 6; Length 25;
Best Local Similarity 57.1%; Pred. No. 1e+05;
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 3 UGAUUDUCATGCGAG 16
Db 21 TGATTTCACTGCGAG 8

RESULT 33
CQ794144/c CQ794144 30 bp DNA linear PAT 19-APR-2004
LOCUS CQ794144
DEFINITION Sequence 64 from Patent EP1403384.
ACCESSION CQ794144
VERSION CQ794144.1 GI:46406786
KEYWORDS
SOURCE human papillomavirus
ORGANISM Human papillomavirus
Papillomaviruses; dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.

REFERENCE
1 Meijer, C.J. and Snijders, P.J.
AUTHORS Method for detecting and typing of cutaneous HPV and primers and
TITLE probes for use therein
JOURNAL Patent: EP 1403384-A 64 31-MAR-2004;
FEATURES Location/Qualifiers
source 1..30
/organism="Human papillomavirus"
/mol_type="unassigned DNA"
/db_xref="taxon:10566"

misc_feature 1..30
/note="probe-binding region in DNA of cutaneous supergroup
B HPV"

ORIGIN

Query Match 72.9%; Score 12.4; DB 6; Length 30;
Best Local Similarity 57.1%; Pred. No. 1e+05;
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCUGAUVUCCAUUGC 14
||:||||:||||
Db 14 CCTGAGTTCATTGC 1

RESULT 34
CQ794148/c 30 bp DNA linear PAT 19-APR-2004
LOCUS Sequence 68 from Patent EP1403384.
DEFINITION CQ794148
ACCESSION CQ794148
VERSION CQ794148.1 GI:46406790
KEYWORDS
SOURCE Human papillomavirus
ORGANISM Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.

REFERENCE 1
AUTHORS Meijer, C.J. and Snijders, P.J.
TITLE Method for detecting and typing of cutaneous HPV and primers and probes for use therein
JOURNAL Patent: EP 1403384-A 68 31-MAR-2004;
Stichting Researchfonds Pathologie (NL)
LOCATION/Qualifiers

FEATURES
source 1..30
/organism="Human papillomavirus"
/mol_type="unassigned DNA"
/db_xref="taxon:10566"
misc_feature 1..30
/note="probe-binding region in DNA of cutaneous supergroup
B HPV"

ORIGIN

Query Match 72.9%; Score 12.4; DB 6; Length 30;
Best Local Similarity 57.1%; Pred. No. 1e+05;
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCUGAUVUCCAUUGC 14
||:||||:||||
Db 14 CCTGAGTTCATTGC 1

RESULT 35
CQ800113/c 30 bp DNA linear PAT 29-APR-2004
LOCUS Sequence 64 from Patent WO2004029302.
DEFINITION CQ800113
ACCESSION CQ800113
VERSION CQ800113.1 GI:46849034
KEYWORDS
SOURCE Human papillomavirus
ORGANISM Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.

REFERENCE 1
AUTHORS Meijer, C.J. and Snijders, P.J.
TITLE Method for detecting and typing of cutaneous HPV and primers and probes for use therein
JOURNAL Patent: WO 2004029302-A 64 08-APR-2004;
Stichting Researchfonds Pathologie (NL)
LOCATION/Qualifiers

FEATURES
source 1..30
/organism="Human papillomavirus"
/mol_type="unassigned DNA"
/db_xref="taxon:10566"
misc_feature 1..30

misc_feature 1..30
/note="probe-binding region in DNA of cutaneous supergroup
B HPV"

ORIGIN

Query Match 72.9%; Score 12.4; DB 6; Length 30;
Best Local Similarity 57.1%; Pred. No. 1e+05;
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCUGAUVUCCAUUGC 14
||:||||:||||
Db 14 CCTGAGTTCATTGC 1

RESULT 36
CQ800117/c 30 bp DNA linear PAT 29-APR-2004
LOCUS Sequence 68 from Patent WO2004029302.
DEFINITION CQ800117
ACCESSION CQ800117
VERSION CQ800117.1 GI:46849038
KEYWORDS
SOURCE Human papillomavirus
ORGANISM Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
Papillomavirus.

REFERENCE 1
AUTHORS Meijer, C.J. and Snijders, P.J.
TITLE Method for detecting and typing of cutaneous HPV and primers and probes for use therein
JOURNAL Patent: WO 2004029302-A 68 08-APR-2004;
Stichting Researchfonds Pathologie (NL)
LOCATION/Qualifiers

FEATURES
source 1..30
/organism="Human papillomavirus"
/mol_type="unassigned DNA"
/db_xref="taxon:10566"
misc_feature 1..30
/note="probe-binding region in DNA of cutaneous supergroup
B HPV"

ORIGIN

Query Match 72.9%; Score 12.4; DB 6; Length 30;
Best Local Similarity 57.1%; Pred. No. 1e+05;
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCUGAUVUCCAUUGC 14
||:||||:||||
Db 14 CCTGAGTTCATTGC 1

RESULT 37
AR171877 49 bp DNA linear PAT 17-DEC-2001
LOCUS AR171877/c
DEFINITION Sequence 10 from patent US 6297365.
ACCESSION AR171877
VERSION AR171877.1 GI:17910827
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 49)
AUTHORS Adams, C.C., Brenhano, S.T. and Schroth, G.P.
TITLE Decoy probes
JOURNAL Patent: US 6297365-A 10 02-OCT-2001;
LOCATION/Qualifiers

FEATURES
source 1..49
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 72.9%; Score 12.4; DB 6; Length 49;
Best Local Similarity 57.1%; Pred. No. 9.8e+04;
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 3 UGAUUDUUCAG 16
:|||||:|||||
DB 25 TGATTTCAGTCAG 12

RESULT 38
LOCUS AR171878 49 bp DNA 11near PAT 17-DEC-2001
DEFINITION Sequence 11 from patent US 6297365.
ACCESSION AR171878
VERSION AR171878.1 GI:17910828
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 49)
AUTHORS Adams,C.C., Brentano,S.T. and Schroth,G.P.
TITLE Decoy probes
JOURNAL Patent: US 6297365-A 11 02-OCT-2001;
FEATURES Location/Qualifiers
source 1..49
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 72.9%; Score 12.4; DB 6; Length 49;
Best Local Similarity 57.1%; Pred. No. 9.8e+04;
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 3 UGAUUDUUCAG 16
:|||||:|||||
DB 25 TGATTTCAGTCAG 12

RESULT 39
LOCUS BD222951 49 bp DNA 11near PAT 17-JUL-2003
DEFINITION Reversible inhibitory probe.
ACCESSION BD222951
VERSION BD222951.1 GI:33032721
KEYWORDS JP 2002521070-A/10.
SOURCE Synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 49)
AUTHORS Adams,C.C., Brentano,S.T. and Schroth,G.P.
TITLE Reversible inhibitory probe
JOURNAL Patent: JP 2002521070-A 10 16-JUL-2002;
COMMENT GEN PROBE INC
OS Synthetic construct
PN JP 2002521070-A/10
PD 16-JUL-2002
PF 30-JUL-1999 JP 2000562561
PR 31-JUL-1998 US 60/094979
PI CHRISTOPHER C ADAMS,STEVEN T BRENTANO,GARY P SCHROTH PC
C12N15/09,C12Q1/68,G01N33/50,C12N15/00
CC Reversible inhibitory probe
FH Key Location/Qualifiers
FT source 1..49
Location/Qualifiers
1..49
/organism='Synthetic construct'.
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match 72.9%; Score 12.4; DB 6; Length 49;
Best Local Similarity 57.1%; Pred. No. 9.8e+04;
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 3 UGAUUDUUCAG 16
:|||||:|||||
DB 25 TGATTTCAGTCAG 12

DB 25 TGATTTCAGTCAG 12

RESULT 40
LOCUS BD222952 49 bp DNA 11near PAT 17-JUL-2003
DEFINITION Reversible inhibitory probe.
ACCESSION BD222952
VERSION BD222952.1 GI:33032722
KEYWORDS JP 2002521070-A/11.
SOURCE Synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 49)
AUTHORS Adams,C.C., Brentano,S.T. and Schroth,G.P.
TITLE Reversible inhibitory probe
JOURNAL Patent: JP 2002521070-A 11 16-JUL-2002;
COMMENT GEN PROBE INC
OS Synthetic construct
PN JP 2002521070-A/11
PD 16-JUL-2002
PF 30-JUL-1999 JP 2000562561
PR 31-JUL-1998 US 60/094979
PI CHRISTOPHER C ADAMS,STEVEN T BRENTANO,GARY P SCHROTH PC
C12N15/09,C12Q1/68,G01N33/50,C12N15/00
CC Reversible inhibitory probe
FH Key Location/Qualifiers
FT source 1..49
Location/Qualifiers
1..49
/organism='Synthetic construct'.
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match 72.9%; Score 12.4; DB 6; Length 49;
Best Local Similarity 57.1%; Pred. No. 9.8e+04;
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 3 UGAUUDUUCAG 16
:|||||:|||||
DB 25 TGATTTCAGTCAG 12

Search completed: May 13, 2005, 18:17:10
Job time : 497.055 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 13, 2005, 16:40:53 ; Search time 123.327 Seconds
(without alignments)
816.004 Million cell updates/sec

Title: US-09-927-046-143
Perfect score: 17
Sequence: 1 ccgaaucaucagcag 17

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues
Total number of hits satisfying chosen parameters: 4530610

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	100.0	17	6	ABK55772 Human CLC
2	16	94.1	17	6	ABK56334 Human CLC
3	16	94.1	17	6	ABK55771 Human CLC
4	15	88.2	15	6	ABK61042 Human CLC
5	15	88.2	15	6	ABK61044 Human CLC
6	15	88.2	15	6	ABK61043 Human CLC
7	15	88.2	15	6	ABK55770 Human CLC
8	15	88.2	15	6	ABK55770 Human CLC
9	14	82.4	15	6	ABK61041 Human CLC
10	14	82.4	17	6	ABK55773 Human CLC
11	14	82.4	19	10	ADG70258 Human CLC
12	13.4	78.8	22	9	ACC70300 Human CLC
13	13.4	78.8	52	12	ADG16067 Human CLC
14	13.4	78.8	66	2	AAT20442 Human CLC
15	13	76.5	15	6	ABK61045 Human CLC
16	13	76.5	17	6	ABK56876 Human CLC
17	13	76.5	17	6	ABK57300 Human CLC
18	13	76.5	43	12	ADP97171 Human CLC
19	13	76.5	60	6	ABN45930 Human CLC
20	12.8	75.3	20	2	AAV51603 Human CLC

21	12.8	75.3	23	2	AAV51602 Human CLC
22	12.8	75.3	25	9	ACK08857 Human CLC
23	12.8	75.3	32	6	ABK33718 Human CLC
24	12.8	75.3	41	2	AAV50992 Human CLC
25	12.8	75.3	41	2	AAV50991 Human CLC
26	12.8	75.3	41	2	AAV50981 Human CLC
27	12.8	75.3	41	2	AAV50994 Human CLC
28	12.8	75.3	41	2	AAV47798 Human CLC
29	12.8	75.3	41	2	AAV47809 Human CLC
30	12.8	75.3	41	2	AAV47788 Human CLC
31	12.8	75.3	63	2	AAH86424 Human CLC
32	12.8	75.3	80	4	AAI27809 Human CLC
33	12.8	75.3	80	4	ABA76122 Human CLC
34	12.8	75.3	80	4	AAI56782 Human CLC
35	12.8	75.3	80	4	ABA40677 Human CLC
36	12.8	75.3	80	4	AAK50790 Human CLC
37	12.8	75.3	80	4	AAK24792 Human CLC
38	12.8	75.3	80	4	ABK50382 Human CLC
39	12.8	75.3	80	6	ABK54274 Human CLC
40	12.8	75.3	100	8	ACD81396 Human CLC
41	12.8	75.3	100	8	ACD78798 Human CLC
42	12.4	72.9	19	11	ADL70081 Human CLC
43	12.4	72.9	19	11	ADL69968 Human CLC
44	12.4	72.9	20	3	AAZ75567 Human CLC
45	12.4	72.9	25	8	AAI52075 Human CLC
46	12.4	72.9	25	13	ADH45223 Human CLC
47	12.4	72.9	27	13	ADR37819 Human CLC
48	12.4	72.9	41	2	AAV47787 Human CLC
49	12.4	72.9	41	2	AAV47796 Human CLC
50	12.4	72.9	41	2	AAV47811 Human CLC
51	12.4	72.9	41	2	AAV47785 Human CLC
52	12.4	72.9	41	2	AAV47795 Human CLC
53	12.4	72.9	47	3	AAZ69384 Human CLC
54	12.4	72.9	49	3	AAZ58532 Human CLC
55	12.4	72.9	49	3	AAZ58531 Human CLC
56	12.4	72.9	60	6	ABN35208 Human CLC
57	12.4	72.9	60	6	ABN42451 Human CLC
58	12.4	72.9	60	6	ABN46050 Human CLC
59	12.4	72.9	65	6	ABN58199 Human CLC
60	12.4	72.9	96	10	ADL01975 Human CLC
61	12.2	71.8	20	2	AAQ37064 Human CLC
62	12.2	71.8	20	12	ADL00821 Human CLC
63	12.2	71.8	20	12	ADL00946 Human CLC
64	12.2	71.8	20	12	ADL00835 Human CLC
65	12.2	71.8	20	12	ADL00820 Human CLC
66	12.2	71.8	23	6	ABT13166 Human CLC
67	12.2	71.8	23	10	ADC42403 Human CLC
68	12.2	71.8	23	10	ADH94249 Human CLC
69	12.2	71.8	24	6	ABK15883 Human CLC
70	12.2	71.8	25	2	AAZ78100 Human CLC
71	12.2	71.8	25	3	AAZ91969 Human CLC
72	12.2	71.8	26	6	ABK559052 Human CLC
73	12.2	71.8	30	3	AAZ28508 Human CLC
74	12.2	71.8	33	6	ABQ84189 Human CLC
75	12.2	71.8	33	6	ABK49706 Human CLC
76	12.2	71.8	37	4	AAH96752 Human CLC
77	12.2	71.8	41	6	ABK48079 Human CLC
78	12.2	71.8	41	6	ABK48080 Human CLC
79	12.2	71.8	41	6	ABL60945 Human CLC
80	12.2	71.8	41	6	ABL60946 Human CLC
81	12.2	71.8	42	12	ADM43116 Human CLC
82	12.2	71.8	42	12	ADM43117 Human CLC
83	12.2	71.8	48	10	ADH08357 Human CLC
84	12.2	71.8	49	10	ADH08358 Human CLC
85	12.2	71.8	51	4	AAI75118 Human CLC
86	12.2	71.8	60	6	ABN33559 Human CLC
87	12.2	71.8	60	6	ABN44704 Human CLC
88	12.2	71.8	60	6	ABN35629 Human CLC
89	12.2	71.8	65	6	ABN58185 Human CLC
90	12.2	71.8	65	6	ABN51685 Human CLC
91	12.2	71.8	88	7	ADK68391 Human CLC
92	12.2	71.8	100	8	ACD79938 Human CLC
93	12.2	71.8	100	8	ACD74179 Human CLC

AAV51602	Zea mays
ACK08857	Human mtc
ABK33718	S. pneumo
AAV50992	Maize pol
AAV50991	Maize pol
AAV50981	Maize pol
AAV50994	Maize pol
AAV47798	Maize pol
AAV47809	Maize pol
AAV47788	Maize pol
AAH86424	Human sln
AAI27809	Probe #17
ABA76122	Human foe
AAI56782	Probe #25
ABA40677	Probe #19
AAK50790	Human bra
AAK24792	Human bra
ABK50382	Human liv
ABK54274	Human gen
ACD81396	E. coli K
ACD78798	E. coli K
ADL70081	Human GIP
ADL69968	Human GIP
AZ75567	Human bla
AAI52075	Escherich
ADH45223	Enterobac
ADR37819	Retinobla
AAV47787	Maize pol
AAV47796	Maize pol
AAV47811	Maize pol
AAV47785	Maize pol
AAV47795	Maize pol
AAZ69384	Human map
AAZ58532	Decoy pro
AAZ58531	Decoy pro
ABN35208	Human spl
ABN42451	Human spl
ABN46050	Human spl
ABN58199	Mouse spl
ADL01975	ATPAlpha
AAQ37064	ADP1 3'
ADL00821	Human VEG
ADL00946	Human VEG
ADL00835	Human VEG
ADL00820	Human VEG
ABT13166	Panc01 a
ADC42403	Human PAN
ADH94249	Human gen
ABK15883	Serratia 1
AAZ78100	Human c-R
AAZ91969	Mehogany
ABK559052	Human G-P
AAZ28508	Primer FO
ABQ84189	P structu
ABK49706	Human kln
AAH96752	Human Cnk
ABK48079	Human zln
ABK48080	Human zln
ABL60945	Tight jun
ABL60946	Tight jun
ADM43116	Rat granz
ADM43117	Rat granz
ADH08357	K. lactis
ADH08358	K. lactis
AAI75118	Human sll
ABN33559	Human spl
ABN44704	Human spl
ABN35629	Human spl
ABN58185	Mouse spl
ABN51685	Mouse spl
ADK68391	Corn seed
ACD79938	E. coli K
ACD74179	E. coli K

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95	12.2	71.8	100	8	ACdF73274	E	coli	K
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97	12.2	71.8	100	8	ACdF74181	E	coli	K
98	12.2	71.8	100	8	ACdF5159	E	coli	K
99	12.2	71.8	100	8	ACdF9539	E	coli	K
100	12	70.6	17	6	ABK56875	Human	CtC	

ALIGNMENTS

RESULT 1

ID ABRK55772 standard; RNA; 17 BP.

XX
AC ABRK55772;
XX
DT 02-JUL-2002 (first entry)
DE Human CLCA1 gene enzymatic nucleic acid #143.
KM Human, chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;
KW antinflammatory; chronic obstructive pulmonary disease; COPD; asthma;
KM chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;
KW oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;
KW acetylcyteline.
OS Homo sapiens.
PN WO200211674-A2.
PP 14-FEB-2002.
PF 09-AUG-2001; 2001WO-US024970.
PR 09-AUG-2000; 2000US-0224383P.
RX
XX
PA (RIBO-) RIBOZYME PHARM INC.
PI (SYNT) SYNTEX USA LLC.
PT (THOM/) THOMPSON J.
PX Thompson J, Mcswiggen J, Mckenzie T, Ayers D, Szymkowski DE;
PY Grube A;
ZZ WPL; 2002-217145/27.

Enzymatic polynucleotide that down regulates expression of chloride channel calcium activated gene, useful for treating Chronic Obstructive pulmonary disease (COPD), chronic bronchitis and asthma.

Claim 4; Page 55; 152pp; English.

The invention relates to enzymatic nucleic acid molecules that down regulate expression of chloride channel calcium activated 1 (CLCA1) genes by cleaving RNA derived from the genes. The nucleic acid sequences are useful as pharmaceutical agents for treating conditions such as chronic obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic fibrosis, obstructive bowel syndrome and any other diseases or conditions that are related to or will respond to the levels of CLCA1 in a cell or tissue. The sequences are useful for reducing CLCA1 activity in a cell, hence, are useful for treatment of a patient having a condition associated with the level of CLCA1, where the invention further comprises the use of one or more therapies under conditions suitable for the treatment, for example, oxygen therapy, bronchodilators, corticosteroids, antibacterials, vaccinations, acetylcysteine and mukocinetik agents. The CC nucleic acids of the invention are also used as diagnostic tools to examine genetic drift and mutations are also used as diagnostic tools to CC the presence of CLCA1 RNA in a cell. This sequence represents an enzymatic nucleic acid molecule of the invention

Sequence 17 BP; 3 A; 4 C; 4 G; 0 T; 6 U; 0 Other;

Query Match	100.0%;	Score 17;	DB 6;	Length 17;
Best Local Similarity	100.0%;	Pred. No. 63;		
Matches 17;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	CCGCAUUCACUUGCAGG	17	
Db	1	CCGCAUUCACUUGCAGG	17	

Query Match	94.1%	Score 16;	DB 6;	Length 17;
Best Local Similarity	100.0%	Fred.No.2.1e+02;		
Matches 16;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY 2 CUGAUUUCAUUGCAG 17
|||||
DB 1 CUGAUUUCAUUGCAG 16

RESULT 3
ABK5771
ID ABK5771 standard; RNA; 17 BP.

AC ABK5771;

DT 02-JUL-2002 (first entry)

DE Human CLCA1 gene enzymatic nucleic acid #142.

XX Human; chloride channel activated 1; CLCA1; ss; antiasthmatic;
KW antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;
KW chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;
KW oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;
KW acetylcysteine.

OS Homo sapiens.

PN WO200211674-A2.

PD 14-FEB-2002.

PR 09-AUG-2001; 2001WO-US024970.

PF 09-AUG-2000; 2000US-0224383P.

PA (RIBO-) RIBOZYME PHARM INC.

PA (SYNT) SYNTEX USA LLC.

PA (THOM/) THOMPSON J.

PI Thompson J, Mcswiggen J, McKenzie T, Ayers D, Szymkowski DE;

PI Grupe A;

PT Enzymatic polynucleotide that down regulates expression of chloride
channel calcium activated gene, useful for treating Chronic obstructive
pulmonary disease (COPD), chronic bronchitis and asthma.

PS Claim 4; Page 55; 152pp; English.

XX The invention relates to enzymatic nucleic acid molecules that down
CC regulate expression of chloride channel calcium activated 1 (CLCA1) genes
CC by cleaving RNA derived from the genes. The nucleic acid sequences are
CC useful as pharmaceutical agents for treating conditions such as chronic
CC obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic
CC fibrosis, obstructive bowel syndrome and any other diseases or conditions
CC that are related to or will respond to the levels of CLCA1 in a cell or
CC tissue. The sequences are useful for reducing CLCA1 activity in a cell,
CC hence, are useful for treatment of a patient having a condition
CC associated with the level of CLCA1, where the invention further comprises
CC the use of one or more therapies under conditions suitable for the
CC treatment, for example, oxygen therapy, bronchodilators, corticosteroids,
CC antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The
CC nucleic acids of the invention are also used as diagnostic tools to
CC examine genetic drift and mutations within diseased cells or to detect
CC the presence of CLCA1 RNA in a cell. This sequence represents an
CC enzymatic nucleic acid molecule of the invention

XX Sequence 17 BP; 3 A; 4 C; 3 G; 0 T; 7 U; 0 Other;

QY Query Match 94.1%; Score 16; DB 6; Length 17;

Best Local Similarity 100.0%; Pred. No. 2.1e+02; Mismatches 0; Gaps 0;

Matches 16; Conservative 0; Indels 0; Gaps 0;

QY 1 CCUGAUUUCAUUGCAG 16
|||||

DB 2 CCUGAUUUCAUUGCAG 17

RESULT 4
ABK61042

ID ABK61042 standard; DNA; 15 BP.

AC ABK61042;

DT 02-JUL-2002 (first entry)

DE Human CLCA1 gene enzymatic nucleic acid #5413.

XX Human; chloride channel activated 1; CLCA1; ss; antiasthmatic;
KW antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;
KW chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;
KW oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;
KW acetylcysteine.

OS Homo sapiens.

PN WO200211674-A2.

PD 14-FEB-2002.

PR 09-AUG-2001; 2001WO-US024970.

PF 09-AUG-2000; 2000US-0224383P.

PA (RIBO-) RIBOZYME PHARM INC.

PA (SYNT) SYNTEX USA LLC.

PA (THOM/) THOMPSON J.

PI Thompson J, Mcswiggen J, McKenzie T, Ayers D, Szymkowski DE;

PI Grupe A;

PT Enzymatic polynucleotide that down regulates expression of chloride
channel calcium activated gene, useful for treating Chronic obstructive
pulmonary disease (COPD), chronic bronchitis and asthma.

PS Claim 4; Page 139; 152pp; English.

XX The invention relates to enzymatic nucleic acid molecules that down
CC regulate expression of chloride channel calcium activated 1 (CLCA1) genes
CC by cleaving RNA derived from the genes. The nucleic acid sequences are
CC useful as pharmaceutical agents for treating conditions such as chronic
CC obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic
CC fibrosis, obstructive bowel syndrome and any other diseases or conditions
CC that are related to or will respond to the levels of CLCA1 in a cell or
CC tissue. The sequences are useful for reducing CLCA1 activity in a cell,
CC hence, are useful for treatment of a patient having a condition
CC associated with the level of CLCA1, where the invention further comprises
CC the use of one or more therapies under conditions suitable for the
CC treatment, for example, oxygen therapy, bronchodilators, corticosteroids,
CC antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The
CC nucleic acids of the invention are also used as diagnostic tools to
CC examine genetic drift and mutations within diseased cells or to detect
CC the presence of CLCA1 RNA in a cell. This sequence represents an
CC enzymatic nucleic acid molecule of the invention

XX Sequence 15 BP; 3 A; 4 C; 2 G; 6 T; 0 U; 0 Other;

QY Query Match 88.2%; Score 15; DB 6; Length 15;

Best Local Similarity 60.0%; Pred. No. 6.7e+02; Mismatches 0; Gaps 0;

Matches 9; Conservative 6; Indels 0; Gaps 0;

QY 1 CCUGAUUUCAUUGCA 15
|||:|:|:|:|:|:|

DB 1 CCTGATTCAATTGCA 15

```

RESULT 5
ABK61043
ID ABK61044 standard; DNA; 15 BP.
AC
XX
XX
AC ABK61044;
XX
XX
DT 02-JUL-2002 (first entry)
XX
XX
DE Human CLCA1 gene enzymatic nucleic acid #5415.
XX
XX
KW Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;
KW antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;
KW chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;
KW oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;
KW acetylcysteine.
XX
XX
OS Homo sapiens.
XX
XX
PN WO200211674-A2.
XX
XX
PD 14-FEB-2002.
XX
XX
PF 09-AUG-2001; 2001WO-US024970.
XX
XX
PR 09-AUG-2000; 2000US-0224383P.
XX
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (SYNT ) SYNTAX USA LLC.
PA (THOM/) THOMPSON J.
XX
XX
PI Thompson J, Mcswiggen J, McKenzie T, Ayers D, Szymkowski DE;
PI Grube A;
XX
XX
DR WPI; 2002-217145/27.
XX
XX
PT Enzymatic polynucleotide that down regulates expression of chloride
PT channel calcium activated gene, useful for treating Chronic obstructive
PT pulmonary disease (COPD), chronic bronchitis and asthma.
XX
XX
PS Claim 4; Page 139; 152pp; English.
XX
XX
CC The invention relates to enzymatic nucleic acid molecules that down
CC regulate expression of chloride channel calcium activated 1 (CLCA1) genes
CC by cleaving RNA derived from the genes. The nucleic acid sequences are
CC useful as pharmaceutical agents for treating conditions such as chronic
CC obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic
CC fibrosis, obstructive bowel syndrome and any other diseases or conditions
CC that are related to or will respond to the levels of CLCA1 in a cell or
CC tissue. The sequences are useful for reducing CLCA1 activity in a cell,
CC hence, are useful for treatment of a patient having a condition
CC associated with the level of CLCA1, where the invention further comprises
CC the use of one or more therapies under conditions suitable for the
CC treatment, for example, oxygen therapy, bronchodilators, corticosteroids,
CC antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The
CC nucleic acids of the invention are also used as diagnostic tools to
CC examine genetic drift and mutations within diseased cells or to detect
CC the presence of CLCA1 RNA in a cell. This sequence represents an
CC enzymatic nucleic acid molecule of the invention
XX
XX
SQ Sequence 15 BP; 3 A; 2 C; 4 G; 6 T; 0 U; 0 Other;
XX
XX
Query Match 88.2%; Score 15; DB 6; Length 15;
Best Local Similarity 60.0%; Pred. NO. 6.7e+02;
Matches 9; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
QY 3 UGAUUCUAGUGCAG 17
DB 1 TGATTTCATTCGAG 15

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XX
XX
AC ABK61043;
XX
XX
DT 02-JUL-2002 (first entry)
XX
XX
DE Human CLCA1 gene enzymatic nucleic acid #5414.
XX
XX
KW Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;
KW antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;
KW chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;
KW oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;
KW acetylcysteine.
XX
XX
OS Homo sapiens.
XX
XX
PN WO200211674-A2.
XX
XX
PD 14-FEB-2002.
XX
XX
PF 09-AUG-2001; 2001WO-US024970.
XX
XX
PR 09-AUG-2000; 2000US-0224383P.
XX
XX
PA (RIBO-) RIBOZYME PHARM INC.
PA (SYNT ) SYNTAX USA LLC.
PA (THOM/) THOMPSON J.
XX
XX
PI Thompson J, Mcswiggen J, McKenzie T, Ayers D, Szymkowski DE;
PI Grube A;
XX
XX
DR WPI; 2002-217145/27.
XX
XX
PT Enzymatic polynucleotide that down regulates expression of chloride
PT channel calcium activated gene, useful for treating Chronic obstructive
PT pulmonary disease (COPD), chronic bronchitis and asthma.
XX
XX
PS Claim 4; Page 139; 152pp; English.
XX
XX
CC The invention relates to enzymatic nucleic acid molecules that down
CC regulate expression of chloride channel calcium activated 1 (CLCA1) genes
CC by cleaving RNA derived from the genes. The nucleic acid sequences are
CC useful as pharmaceutical agents for treating conditions such as chronic
CC obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic
CC fibrosis, obstructive bowel syndrome and any other diseases or conditions
CC that are related to or will respond to the levels of CLCA1 in a cell or
CC tissue. The sequences are useful for reducing CLCA1 activity in a cell,
CC hence, are useful for treatment of a patient having a condition
CC associated with the level of CLCA1, where the invention further comprises
CC the use of one or more therapies under conditions suitable for the
CC treatment, for example, oxygen therapy, bronchodilators, corticosteroids,
CC antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The
CC nucleic acids of the invention are also used as diagnostic tools to
CC examine genetic drift and mutations within diseased cells or to detect
CC the presence of CLCA1 RNA in a cell. This sequence represents an
CC enzymatic nucleic acid molecule of the invention
XX
XX
SQ Sequence 15 BP; 3 A; 3 C; 3 G; 6 T; 0 U; 0 Other;
XX
XX
Query Match 88.2%; Score 15; DB 6; Length 15;
Best Local Similarity 60.0%; Pred. NO. 6.7e+02;
Matches 9; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
QY 2 CUGAUUCUAGUGCAG 16
DB 1 CTGATTTCATTCGAG 15

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RESULT 6
ABK61043
ID ABK61043 standard; DNA; 15 BP.

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RESULT 7
ABK55770
ID ABK55770 standard; RNA; 17 BP.

```

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AC
XX
AC ABK55770;
XX

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02-JUL-2002 (first entry)
Human CLCA1 gene enzymatic nucleic acid #141.
Human; chloride channel, calcium activated 1; CLCA1; ss; antiasthmatic;
antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;
chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;
oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;
acetylcysteine.
Homo sapiens.
WO200211674-A2.
14-FEB-2002.
09-AUG-2001; 2001WO-US024970.
09-AUG-2000; 2000US-0224383P.
(RIBO-) RIBOZYME PHARM INC.
(SYNT) SYNTEX USA LLC.
(THOM/) THOMPSON J.
Thompson J, Mcswigen J, McKenzie T, Ayers D, Szymkowski DE;
Grube A;
WPI; 2002-217145/27.
Enzymatic polynucleotide that down regulates expression of chloride
channel calcium activated gene, useful for treating chronic obstructive
pulmonary disease (COPD), chronic bronchitis and asthma.
Claim 4; Page 55; 152pp; English.
The invention relates to enzymatic nucleic acid molecules that down
regulate expression of chloride channel calcium activated 1 (CLCA1) genes
by cleaving RNA derived from the genes. The nucleic acid sequences are
useful as pharmaceutical agents for treating conditions such as chronic
obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic
fibrosis, obstructive bowel syndrome and any other diseases or conditions
that are related to or will respond to the levels of CLCA1 in a cell or
tissue. The sequences are useful for reducing CLCA1 activity in a cell,
hence, are useful for treatment of a patient having a condition
associated with the level of CLCA1, where the invention further comprises
the use of one or more therapies under conditions suitable for the
treatment, for example, oxygen therapy, bronchodilators, corticosteroids,
antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The
nucleic acids of the invention are also used as diagnostic tools to
examine genetic drift and mutations within diseased cells or to detect
the presence of CLCA1 RNA in a cell. This sequence represents an
enzymatic nucleic acid molecule of the invention
Sequence 17 BP; 3 A; 5 C; 2 G; 0 T; 7 U; 0 Other;
Query Match 88.2%; Score 15; DB 6; Length 17;
- Best Local Similarity 100.0%; Pred. No. 6; 8e-02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCUGAUVUUGCA 15
Db 3 CCUGAUVUUGCA 17
RESULT 8
ABSI7908
ID ABSI7908 standard; DNA; 88 BP.
XX ABSI7908;
AC
XX
XX 19-AUG-2002 (first entry)
DT
XX
DE Human genome-derived single exon probe ORF from lung SEQ ID No 17899.

Human; ds; single exon probe; asthma; lung cancer; COPD; ILD;
chronic obstructive pulmonary disease; interstitial lung disease;
familial idiopathic pulmonary fibrosis; neurofibromatosis;
tuberculous sclerotic; Gaucher's disease; Niemann-Pick disease;
Hernansky-Rudrak syndrome; sarcoidosis; pulmonary haemoliderosis;
pulmonary histiocytosis; lymphangioleiomyomatosis; Karsenger syndrome;
pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
primary ciliary dyskinesia; pulmonary hypertension;
hyaline membrane disease; open reading frame; ORF.
Homo sapiens.
WO200186003-A2.
15-NOV-2001.
30-JAN-2001; 2001WO-US000665.
04-FEB-2000; 2000US-0180312P.
26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
(MOLE-) MOLECULAR DYNAMICS INC.
Penn SG, Hanzel DK, Chen W, Rank DR;
WPI; 2002-114183/15.
Spatially-addressable set of single exon nucleic acid probes, used to
measure gene expression in human lung samples.
Claim 4; SEQ ID NO 17899; 634pp; English.
The invention relates to a spatially-addressable set of single exon
nucleic acid probes for measuring gene expression in a sample derived
from human lung comprising single exon nucleic acid probes having one of
12614 nucleic acid sequences mentioned in the specification, or their
complements or the 12387 open reading frames derived from the 12614
probes. Also included are a microarray comprising the novel set of probes
; the novel set of probes which hybridise at high stringency to a nucleic
acid expressed in the human lung; measuring gene expression in a sample
derived from human lung, comprising (a) contacting the array with a
collection of detectably labeled nucleic acids derived from human lung
mRNA, and (b) measuring the label detectably bound to each probe of the
array; identifying exons in a eukaryotic genome, comprising (a)
algorithmically predicting at least one exon from genomic sequences of
the eukaryote; and (b) detecting specific hybridisation of detectably
labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
having a fragment identical to the predicted exon, the probe is included
in the above mentioned microarray; assigning exons to a single gene,
comprising (a) identifying exons from genomic sequence by the method
above and (b) measuring the expression of each of the exons in several
tissues and/or cell types using hybridisation to a single exon
microarrays having a probe with the exon, where a common pattern of
expression of the exons in the tissues and/or cell types indicates that
the exons should be assigned to a single gene; a peptide comprising one
of 12011 sequences, mentioned in the specification, or encoded by the
probes/open reading frames (ORF). The probes are used for gene expression
analysis, and for identifying exons in a gene, particularly using human
lung derived mRNA and for the study of lung diseases such as asthma, lung
cancer, chronic obstructive pulmonary disease (COPD), interstitial lung
disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,
tuberculous sclerotic, Gaucher's disease, Niemann-Pick disease, Hernansky-
Rudrak syndrome, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,
histiocytosis, fibrocystic pulmonary dysplasia, primary ciliary
dyskinesia, pulmonary hypertension and hyaline membrane disease. The
present sequence is a single exon probe open reading frame of the

CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at http://wipo.int/publ/published_pct_sequences
XX

XX Sequence 88 BP; 27 A; 24 C; 12 G; 25 T; 0 U; 0 Other;
SQ

Query Match 88.2%; Score 15; DB 6; Length 88;
Best Local Similarity 60.0%; Pred. No. 7.8e+02;
Matches 9; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCUGAUVUUCAGCA 15
DB 63 CCTGATTTCATTGCA 77

RESULT 9
ABK61041
ID ABK61041 standard; DNA; 15 BP.
XX
XX ABK61041;
AC
XX
XX 02-JUL-2002 (first entry)
DT
XX
XX Human CLCA1 gene enzymatic nucleic acid #5412.
DE
XX
XX Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;
KW
XX
XX antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;
KW
XX
XX chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;
KW
XX
XX oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;
KW
XX
XX acetylcysteine.
XX
XX
XX Homo sapiens.
OS
XX
XX WO200211674-A2.
PN
XX
XX 14-FEB-2002.
PD
XX
XX 09-AUG-2001; 2001WO-US024970.
PF
XX
XX 09-AUG-2000; 2000US-0224383P.
PR
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA
XX
XX (SYNT) SYNTEX USA LLC.
PA
XX
XX (THOM/) THOMPSON J.
PA
XX
XX Thompson J, Mcswigen J, McKenzie T, Ayers D, Szymkowski DE;
PI
XX
XX Gruppe A;
PI
XX
XX WPI; 2002-217145/27.
DR
XX
XX Enzymatic polynucleotide that down regulates expression of chloride
PT
XX
XX channel calcium activated gene, useful for treating Chronic obstructive
PT
XX
XX pulmonary disease (COPD), chronic bronchitis and asthma.
PS
XX
XX Claim 4; Page 138; 152pp; English.

CC The invention relates to enzymatic nucleic acid molecules that down
CC regulate expression of chloride channel calcium activated 1 (CLCA1) genes
CC by cleaving RNA derived from the genes. The nucleic acid sequences are
CC useful as pharmaceutical agents for treating conditions such as chronic
CC obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic
CC fibrosis, obstructive bowel syndrome and any other diseases or conditions
CC that are related to or will respond to the levels of CLCA1 in a cell or
CC tissue. The sequences are useful for reducing CLCA1 activity in a cell,
CC hence, are useful for treatment of a patient having a condition
CC associated with the level of CLCA1, where the invention further comprises
CC the use of one or more therapies under conditions suitable for the
CC treatment, for example, oxygen therapy, bronchodilators, corticosteroids,
CC antibiotics, vaccinations, acetylcysteine and mucokinetic agents. The
CC nucleic acids of the invention are also used as diagnostic tools to
CC examine genetic drift and mutations within diseased cells or to detect
CC the presence of CLCA1 RNA in a cell. This sequence represents an
CC enzymatic nucleic acid molecule of the invention

XX
SQ Sequence 15 BP; 2 A; 4 C; 2 G; 7 T; 0 U; 0 Other;
XX

Query Match 82.4%; Score 14; DB 6; Length 15;
Best Local Similarity 57.1%; Pred. No. 2.2e+03;
Matches 8; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCUGAUVUUCAGUC 14
DB 2 CCTGATTTCATTGC 15

RESULT 10
ABK5773
ID ABK5773 standard; RNA; 17 BP.
XX
XX ABK5773;
AC
XX
XX 02-JUL-2002 (first entry)
DT
XX
XX Human CLCA1 gene enzymatic nucleic acid #144.
DE
XX
XX Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;
KW
XX
XX antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;
KW
XX
XX chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;
KW
XX
XX oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;
KW
XX
XX acetylcysteine.
XX
XX
XX Homo sapiens.
OS
XX
XX WO200211674-A2.
PN
XX
XX 14-FEB-2002.
PD
XX
XX 09-AUG-2001; 2001WO-US024970.
PF
XX
XX 09-AUG-2000; 2000US-0224383P.
PR
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA
XX
XX (SYNT) SYNTEX USA LLC.
PA
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XX (THOM/) THOMPSON J.
PA
XX
XX Thompson J, Mcswigen J, McKenzie T, Ayers D, Szymkowski DE;
PI
XX
XX Gruppe A;
PI
XX
XX WPI; 2002-217145/27.
DR
XX
XX Enzymatic polynucleotide that down regulates expression of chloride
PT
XX
XX channel calcium activated gene, useful for treating Chronic obstructive
PT
XX
XX pulmonary disease (COPD), chronic bronchitis and asthma.
PS
XX
XX Claim 4; Page 55; 152pp; English.

CC The invention relates to enzymatic nucleic acid molecules that down
CC regulate expression of chloride channel calcium activated 1 (CLCA1) genes
CC by cleaving RNA derived from the genes. The nucleic acid sequences are
CC useful as pharmaceutical agents for treating conditions such as chronic
CC obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic
CC fibrosis, obstructive bowel syndrome and any other diseases or conditions
CC that are related to or will respond to the levels of CLCA1 in a cell or
CC tissue. The sequences are useful for reducing CLCA1 activity in a cell,
CC hence, are useful for treatment of a patient having a condition
CC associated with the level of CLCA1, where the invention further comprises
CC the use of one or more therapies under conditions suitable for the
CC treatment, for example, oxygen therapy, bronchodilators, corticosteroids,
CC antibiotics, vaccinations, acetylcysteine and mucokinetic agents. The
CC nucleic acids of the invention are also used as diagnostic tools to
CC examine genetic drift and mutations within diseased cells or to detect
CC the presence of CLCA1 RNA in a cell. This sequence represents an
CC enzymatic nucleic acid molecule of the invention

Sequence 17 BP; 6 A; 2 C; 4 G; 0 T; 5 U; 0 Other;

Enzymatic polynucleotide that down regulates expression of chloride channel calcium activated gene, useful for treating Chronic obstructive pulmonary disease (COPD), chronic bronchitis and asthma.

Claim 4, Page 111, 152pp, English.

The invention relates to enzymatic nucleic acid molecules that down regulate expression of chloride channel calcium activated 1 (CLCA1) genes by cleaving RNA derived from the genes. The nucleic acid sequences are useful as pharmaceutical agents for treating conditions such as chronic obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic fibrosis, obstructive bowel syndrome and any other diseases or conditions that are related to or will respond to the levels of CLCA1 in a cell or tissue. The sequences are useful for reducing CLCA1 activity in a cell, hence, are useful for treatment of a patient having a condition associated with the level of CLCA1, where the invention further comprises the use of one or more therapies under conditions suitable for the treatment, for example, oxygen therapy, bronchodilators, corticosteroids, antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The nucleic acids of the invention are also used as diagnostic tools to examine genetic drift and mutations within diseased cells or to detect the presence of CLCA1 RNA in a cell. This sequence represents an enzymatic nucleic acid molecule of the invention

Sequence 17 BP, 3 A, 5 C, 2 G, 0 T, 7 U, 0 Other;

Query Match 76.5%; Score 13; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 7.3e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CCUGAUTCACUG 13
|||||
5 CCUGAUTCACUG 17

RESURF 18
ADP97171/C
ADP97171 standard; DNA, 43 BP.

ADP97171;
23-SEP-2004 (first entry)

C. albicans specific gene,orf6.3991, knockout downstream primer.

Diploid fungal cell; allele; gene disruption cassette;
promoter replacement fragment; antifungal; fungicide; gene therapy;
infection; Candida albicans; knockout; primer; ss.

Candida albicans.
Unidentified.

WO2004056965-A2.

08-JUL-2004.

19-DEC-2003; 2003WO-US040618.

19-DEC-2002; 2002US-0434832P.

(ELIT-) ELITRA PHARM INC.
(ELIT-) ELITRA CANADA LTD.

Roemer T, Jiang B, Boone C, Bussey H;
WPI; 2004-500296/47.

Constructing a strain of diploid fungal cells in which both alleles of a gene are modified comprises modifying the alleles of a gene in the fungal cells by recombination using a gene disruption cassette and a promoter replacement fragment.

Claim 76; SEQ ID NO 1206; 163pp; English.

The invention relates to a novel method for constructing a strain of diploid fungal cells in which both alleles of a gene are modified. The method comprises modifying the alleles of a gene in diploid fungal cells by recombination using a gene disruption cassette and a promoter replacement fragment. The invention further comprises: assembling a collection of diploid fungal cells each of which comprises modified alleles of a different gene; a strain of diploid fungal cells comprising modified alleles of a gene, where the first allele of the gene is inactivated by a gene disruption cassette comprising a nucleotide sequence encoding an expressible selectable marker; and the expression of the second allele of the gene is regulated by a heterologous promoter that is operably linked to the coding region of the second allele of the gene, and where the gene encodes the polypeptide mentioned above; a collection of diploid fungal strains comprising the diploid strains cited above, where substantially all the different genes that encode the above amino acid sequences are modified and are present in different diploid strains in the collection; a nucleic acid molecule microarray comprising nucleic acid molecules, where each nucleic acid molecule comprises a nucleotide sequence that is hybridizable to a target nucleotide sequence comprising any of the 310 nucleotide sequences listed in the specification (ADP98516-ADP98825); identifying a gene that is essential to the survival or growth of a fungus, that contributes to the virulence and/or pathogenicity of a fungus, or that contributes to the resistance of a diploid fungus to an antifungal agent; identifying an antifungal agent that inhibits the growth of a diploid fungus, or a therapeutic agent for treatment of a mammalian disease; correlating changes in the levels of proteins or gene transcripts with the inhibition of growth or proliferation of a diploid fungal cell; a purified or isolated nucleic acid molecule comprising a nucleotide sequence encoding a gene product required for proliferation of Candida albicans, where the gene product consists of any of the above-mentioned amino acid sequences; a vector comprising a promoter operably linked to the nucleic acid molecule cited above; a host cell containing the vector; a purified or isolated polypeptide comprising any of the 61 amino acid sequences given in the specification (ADP96718-ADP96778); a fusion protein comprising a fragment of a first polypeptide fused to a second polypeptide, the fragment consisting of at least 6 consecutive residues of any of ADP98826-ADP99135; producing a polypeptide; identifying a compound which modulates the activity of a gene product encoded by a nucleic acid comprising any of ADP98516-ADP98825; eliciting an immune response in an animal; a strain of Candida albicans, where a first allele of a gene comprising any of ADP98516-ADP98825 is inactive and a second allele of the gene is under the control of a heterologous promoter; identifying a compound or binding partner that binds to the polypeptide comprising any of ADP98826-ADP99135, or its fragment; identifying a compound having the ability to inhibit growth or proliferation of Candida albicans; inhibiting growth or proliferation of Candida albicans cells; manufacturing an antimycotic compound; treating an infection of a subject by Candida albicans; preventing or containing contamination of an object by Candida albicans, or for preventing or inhibiting formation on a surface of a biofilm comprising Candida albicans; a pharmaceutical composition comprising a therapeutic amount of an agent which reduces the activity or level of a gene product encoded by a nucleic acid comprising any of ADP98516-ADP98825 in a pharmaceutical carrier; an antibody preparation which binds to the polypeptide; methods for evaluating a compound against a target gene product encoded by any of ADP98516-ADP98825; identifying an antimycotic compound; a computer or a computer readable medium that comprises at least one of the nucleotide sequences mentioned in the specification or at least one amino acid sequence selected from ADP98826-ADP99135; a method assisted by a computer for identifying a putatively essential gene of a fungus; and a protein array comprising proteins, where at least one protein comprises an amino acid sequence or a portion of an amino acid sequence selected from ADP98516-ADP98825. The novel methods and compositions have fungicide activity. The compositions may be used in gene therapy. The composition and methods are useful for drug screening purposes or for diagnosing, preventing or treating infections associated with Candida albicans. These may also be used for constructing strains useful for identification and validation of gene products as effective targets for therapeutic intervention, for identifying and validating gene products as effective targets for therapeutic intervention, and for collecting identified essential genes. This polynucleotide sequence represents a knockout primer used in the exemplification of the

CC invention. NOTE: This sequence was downloaded from an electronic sequence
CC listing provided on the WIPO website.
XX
SQ Sequence 43 BP; 19 A; 7 C; 5 G; 12 T; 0 U; 0 Other;
Query Match 76.5%; Score 13; DB 12; Length 43;
Best Local Similarity 53.8%; Pred. No. 7.9e+03;
Matches 7; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCUGAUNUCAG 13
||:|:|:|:|:|:|
DB 22 CCGATTCATTCG 10
RESULT 19
ABN45930
ID ABN45930 standard; DNA; 60 BP.
XX
AC ABN45930;
XX
DT 15-JUL-2002 (first entry)
XX
DE Human spliced transcript detection oligonucleotide SEQ ID NO:18678.
XX
KW Human; mouse; rat; splice transcript; detection; RNA transcript;
KW splice variant; transcriptome; oligonucleotide library; ss.
XX
OS Homo sapiens.
XX
PN WO200210449-A2.
XX
PD 07-FEB-2002.
XX
PF 20-JUL-2001; 2001WO-1B001903.
XX
PR 28-JUL-2000; 2000US-0221607P.
PR 02-MAY-2001; 2001US-0287724P.
XX
PA (COMP-) COMPUGEN INC.
XX
PI Shoshan A, Wasserman A, Mintz E, Mintz L, Faigler S;
XX
DR WPI; 2002-257383/30.
XX
PT New oligonucleotide libraries comprising oligonucleotides which
PT selectively hybridize to mRNAs transcribed from a transcription unit of a
PT genome, useful for detecting tissue-, pathology-, and developmental-
PT specific genes.
XX
PS Example 1; SEQ ID NO 18678; 47pp; English.
XX
CC The present invention describes oligonucleotide libraries for detecting
CC messenger RNAs that populate a (sub-)transcriptome, where the (sub-
CC)transcriptome comprises messenger RNAs transcribed from multiple
CC transcription units that populate a genome. The library comprises several
CC oligonucleotides, each capable of hybridizing selectively to a set of
CC messenger RNAs transcribed from a given transcription unit of the genome,
CC which encodes one or more messenger RNA splice variants. The
CC oligonucleotide libraries are useful for detecting mRNAs from a
CC biological sample, in expression profiling studies, in qualitatively or
CC quantitatively characterizing the corresponding transcriptome, and in
CC detecting RNA transcripts and splice variants of human or animal
CC transcriptomes. The libraries may also be used as specialised mini
CC libraries to detect transcripts of a sub-transcriptome under a particular
CC biological or pathological state, and so allowing the detection of
CC - and pathology-specific genes such as those genes only expressed in
CC specific tissue under a specific pathological condition; to detect
CC developmental specific genes; and to detect RNA transcripts and splice
CC variants of a transcriptome of a patient suffering from a particular
CC disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from
CC rats, humans and mice, which are used in the exemplification of the
CC present invention. N.B. The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format

CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 60 BP; 23 A; 11 C; 13 G; 13 T; 0 U; 0 Other;
Query Match 76.5%; Score 13; DB 6; Length 60;
Best Local Similarity 61.5%; Pred. No. 8.1e+03;
Matches 8; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
QY 4 GAUUCAUUCGAG 16
||:|:|:|:|:|:|
DB 30 GATTTCATTCGAG 42
RESULT 20
AAV51603
ID AAV51603 standard; DNA; 20 BP.
XX
AC AAV51603;
XX
DT 02-FEB-1999 (first entry)
XX
DE Zea mays genome forward PCR primer #203.
XX
KW Polymorphic marker; allele-specific; probe; amplification; PCR primer;
KW hybridisation; plant; hybrid certification; genetic contribution;
KW progeny; back-cross; hybrid; ancestry; corn; ss.
XX
OS Synthetic.
XX
PN Zea mays.
XX
PD WO9824796-A1.
XX
PF 11-JUN-1998.
XX
PR 01-DEC-1997; 97WO-US021782.
XX
PR 02-DEC-1996; 96US-0032069P.
PR 07-MAR-1997; 97US-00813507.
XX
PA (AFRY-) AFFYMETRIX INC.
XX
PI Lemieux B, Landry BS, Sapolsky RJ, Murgieux A;
XX
DR WPI; 1998-333252/29.
XX
PT Brassica species allele-specific oligonucleotide probes and primers -
PT useful for plant breeding.
XX
PS Example 1; Page 53; 65pp; English.
XX
CC AAV51401-US1704 are forward PCR primers used to amplify fragments of the
CC Zea mays genome in order to detect polymorphic markers. Such markers can
CC be used in the construction of allele-specific primers and probes for
CC amplification or hybridisation, e.g. to determine common or disparate
CC ancestry between 2 or more plants, to monitor the genetic contribution of
CC an ancestral plant, to trace the progeny of proprietary plants, in
CC certification of a hybrid plant or to identify the progeny of a back-
CC crossed plant with an ancestral plant
XX
SQ Sequence 20 BP; 4 A; 5 C; 4 G; 7 T; 0 U; 0 Other;
Query Match 75.3%; Score 12.8; DB 2; Length 20;
Best Local Similarity 56.2%; Pred. No. 9.4e+03;
Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
QY 1 CCUGAUNUCAG 16
||:|:|:|:|:|:|
DB 2 CTTGATTCATTCGAG 17
RESULT 21
AAV51602
ID AAV51602 standard; DNA; 23 BP.

```
XX AC AAV51602;
XX PF
XX DT 02-FEB-1999 (first entry)
XX DE Zea mays genome forward PCR primer #202.
XX KM Polymorphic marker; allele-specific; probe; amplification; PCR primer;
XX KM hybridisation; plant; hybrid certification; genetic contribution;
XX KM progeny; back-cross; hybrid; ancestry; corn; ss.
XX OS Synthetic.
XX OS Zea mays.
XX PN WO9824796-A1.
XX PD 11-JUN-1998.
XX PF 01-DEC-1997; 97WO-US021782.
XX PR 02-DEC-1996; 96US-0032069P.
XX PR 07-MAR-1997; 97US-00813507.
XX PA (AFRY-) AFFYMETRIX INC.
XX PI Lemieux B, Landry BS, Sapolsky RJ, Murigneux A;
XX DR WPI, 1998-333252/29.
XX PT Braasia species allele-specific oligonucleotide probes and primers -
XX PT useful for plant breeding.
XX PS Example 1; Page 53; 65pp; English.
XX CC AAV51401-US1704 are forward PCR primers used to amplify fragments of the
XX CC Zea mays genome in order to detect polymorphic markers. Such markers can
XX CC be used in the construction of allele-specific primers and probes for
XX CC amplification or hybridisation, e.g. to determine common or disparate
XX CC ancestry between 2 or more plants, to monitor the genetic contribution of
XX CC an ancestral plant, to trace the progeny of proprietary plants, in
XX CC certification of a hybrid plant or to identify the progeny of a back-
XX CC crossed plant with an ancestral plant
XX SQ Sequence 23 BP; 5 A; 5 C; 5 G; 8 T; 0 U; 0 Other;
Query Match 75.3%; Score 12.8; DB 2; Length 23;
Best Local Similarity 56.2%; Pred. No. 9.5e+03;
Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
QY 1 CCUGAUUUCAUUGCAG 16
Db 5 CTTGATTCATTCGAG 20
RESULT 22
ACK08857
ID ACK08857 standard; DNA; 25 BP.
XX AC ACK08857;
XX DT 14-OCT-2003 (first entry)
XX DE Human microarray DNA oligonucleotide SEQ ID NO 108838.
XX KM EST, ss; probe; expressed sequence tag; microarray; gene expression;
XX KM genetic variation; diallelic marker; polymorphism; human;
XX KM cross-species comparison.
XX OS Homo sapiens.
XX OS US2003104410-A1.
XX PN
XX PD 05-JUN-2003.
```

```
XX PF 15-MAR-2002; 2002US-00098263.
XX PR 16-MAR-2001; 2001US-0276759P.
XX PA (AFRY-) AFFYMETRIX INC.
XX PI Miltmann MP;
XX DR WPI, 2003-567953/53.
XX PT New array of nucleic acid probes, useful for in situ hybridization, in
XX PT Southern, Northern or dot-blot hybridization to identify or detect the
XX PT sequence or specific mutations of any gene.
XX PS Claim 1; SEQ ID NO 108838; 9pp; English.
XX CC The invention discloses a microarray comprising a plurality of nucleic
XX CC acid probes including one of 2,018,500 fully defined sequences, or its
XX CC perfect match, perfect mismatch, antisense match or antisense mismatch.
XX CC Also disclosed is a method of gene expression analysis. The array is used
XX CC in monitoring gene expression levels by hybridisation to a DNA library,
XX CC in analysis of genetic variation or in hybridisation of tag-labelled
XX CC compounds. The nucleic acid probes are specifically designed for analysis
XX CC of at least one target sequence. The method of analysis comprises
XX CC hybridising at least one or more nucleic acids to at least two or more
XX CC nucleic acid probes and detecting the hybridisation. The nucleic acid
XX CC probes are attached to a solid support. The analysis comprises monitoring
XX CC gene expression levels, identifying diallelic markers or polymorphisms,
XX CC or family members of a gene and a cross-species comparison. Each of the
XX CC nucleic acids further comprises a tag sequence. The array of nucleic acid
XX CC probes is useful in situ hybridisation, in Southern, Northern or dot-
XX CC blot hybridisation to identify or detect the sequence or specific
XX CC mutations of any gene, in mapping the 5' termini of mRNA molecules by
XX CC primer extensions or in screening cDNA or genomic libraries or subclones
XX CC for additional subclones containing segments of DNA that have been
XX CC isolated and previously sequenced. The sequence presented is one of the
XX CC nucleic acid probes incorporated in the microarray. Note: The sequence
XX CC data for this patent can also be obtained in electronic format directly
XX CC from USPTO at seqdata.uspto.gov/sequence.html
XX SQ Sequence 25 BP; 9 A; 5 C; 4 G; 7 T; 0 U; 0 Other;
Query Match 75.3%; Score 12.8; DB 9; Length 25;
Best Local Similarity 56.2%; Pred. No. 9.5e+03;
Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
QY 1 CCUGAUUUCAUUGCAG 16
Db 9 CCAGATTCATTCGAG 24
RESULT 23
ABK33718/c
ID ABK33718 standard; DNA; 32 BP.
XX AC ABK33718;
XX DT 08-MAY-2002 (first entry)
XX DE S. pneumoniae BVH-3 gene, PCR primer HAMJ 359.
XX KM BVH-3; BVH-11; vaccine; meningitis; otitis media; bacteraemia; pneumonia;
XX KM streptococcal bacterial infection; PCR; primer; ss.
XX OS Streptococcus pneumoniae.
XX OS WO200198334-A2.
XX PN
XX PD 27-DEC-2001.
XX PF 19-JUN-2001; 2001WO-CA000908.
```

PR 20-JUN-2000; 2000US-0212683P.
 XX (SHIR-) SHIRE BIOCHEM INC.
 XX
 XX Hamel J, Quellet C, Charland N, Martin D, Brodeur B;
 PI WPI, 2002-122272/16.
 XX
 XX New Streptococcus pneumoniae BVH-3 and BVH-11 variant and epitope-bearing
 PT polypeptides, useful as vaccine components for treating or preventing
 PT streptococcal infections such as otitis media, meningitis, and
 PT bacteraemia.
 XX
 XX Example 1; Page 33; 113pp; English.
 PS
 XX The invention describes an isolated polypeptide (I) with 70-90% identity
 CC to Streptococcus pneumonia protein BVH-3, BVH-11, variance of BVH-3 or
 CC BVH-11, or chimeric sequences derived from them. A vaccine (II)
 CC comprising (I) is useful for therapeutic or prophylactic treatment of
 CC meningitis, otitis media, bacteraemia or pneumonia infection in an
 CC individual susceptible to these disorders. (II) is also useful for
 CC therapeutic or prophylactic treatment of any streptococcal bacterial
 CC infection (e.g., caused by Streptococcus pneumoniae, group A
 CC Streptococcus such as Streptococcus pyogenes, group B Streptococcus such
 CC as Streptococcus agalactiae, S. dysgalactiae, S. uberis, S. nodocidia or
 CC Staphylococcus aureus) in an individual susceptible to the infection. A
 CC polynucleotide (III) encoding (I) is useful in DNA immunisation.
 CC techniques. The Streptococcus polypeptides are useful in a diagnostic
 CC test for S. pneumoniae infection. (III) is useful for designing DNA
 CC probes for use in detecting the presence of Streptococcus in a biological
 CC sample suspected of containing the bacteria. The DNA probes may also be
 CC used for detecting circulating S. pneumonia nucleic acid in a sample for
 CC diagnosing streptococcal infections. This sequence represents a primer
 CC used for the isolation of S. pneumoniae genes from which the antigenic
 CC peptides of the invention are derived
 CC
 XX
 SQ Sequence 32 BP; 9 A; 10 C; 6 G; 7 T; 0 U; 0 Other;
 Query Match 75.3%; Score 12.8; DB 6; Length 32;
 Best Local Similarity 56.2%; Pred. No. 9.8e+03;
 Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
 OY 2 CUGAUVUUCAGCAG 17
 DB 24 CTGATTTCATAGCGG 9
 RESULT 24
 AAV50992
 ID AAV50992 standard; DNA; 41 BP.
 XX
 AC AAV50992;
 XX
 XX 04-JAN-1999 (first entry)
 DT
 XX
 XX Maize polymorphic marker S43G1/G4-1 DNA.
 DE
 XX
 XX Polymorphic marker; allele-specific; primer; probe; amplification;
 KW hybridisation; plant; hybrid certification; genetic contribution;
 KW progeny; back-cross; hybrid; ancestry; maize; ss.
 XX
 XX Zea mays.
 OS
 XX
 XX Key Location/Qualifiers
 FH variation 21
 FT /*tag= a
 FT /replace= a
 FT /note= "polymorphism"
 XX
 XX MO9824796-A1.
 XX 11-JUN-1998.
 XX

PF 01-DEC-1997; 97WO-US021782.
 XX
 XX 02-DEC-1996; 96US-0032069P.
 PR 07-MAR-1997; 97US-00813507.
 XX
 XX (AFFY-) AFFYMETRIX INC.
 PA
 XX
 XX Lemieux B, Landry BS, Sapolsky RJ, Murgineux A;
 PI WPI, 1998-333252/29.
 XX
 XX Brassica species allele-specific oligonucleotide probes and primers -
 PT useful for plant breeding.
 XX
 XX Claim 1; Page 43; 65pp; English.
 PS
 XX This DNA sequence is a region of a Zea mays genome which contains a
 CC polymorphic marker. This sequence can be used in the construction of
 CC allele-specific primers and probes for amplification or hybridisation,
 CC e.g. to determine common or disparate ancestry between 2 or more plants,
 CC to monitor the genetic contribution of an ancestral plant, to trace the
 CC progeny of proprietary plants, in certification of a hybrid plant or to
 CC identify the progeny of a back-crossed plant with an ancestral plant
 CC
 XX
 SQ Sequence 41 BP; 9 A; 10 C; 14 G; 8 T; 0 U; 0 Other;
 Query Match 75.3%; Score 12.8; DB 2; Length 41;
 Best Local Similarity 56.2%; Pred. No. 1e+04;
 Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
 OY 1 CCUGAUVUUCAGCAG 16
 DB 1 CTTGATTTCATGCG 16
 RESULT 25
 AAV50971
 ID AAV50971 standard; DNA; 41 BP.
 XX
 AC AAV50971;
 XX
 XX 04-JAN-1999 (first entry)
 DT
 XX
 XX Maize polymorphic marker S43G2/G6-2B DNA.
 DE
 XX
 XX Polymorphic marker; allele-specific; primer; probe; amplification;
 KW hybridisation; plant; hybrid certification; genetic contribution;
 KW progeny; back-cross; hybrid; ancestry; maize; ss.
 XX
 XX Zea mays.
 OS
 XX
 XX Key Location/Qualifiers
 FH variation 21
 FT /*tag= a
 FT /replace= g
 FT /note= "polymorphism"
 XX
 XX MO9824796-A1.
 XX 11-JUN-1998.
 XX
 XX 01-DEC-1997; 97WO-US021782.
 PF
 XX
 XX 02-DEC-1996; 96US-0032069P.
 PR 07-MAR-1997; 97US-00813507.
 XX
 XX (AFFY-) AFFYMETRIX INC.
 PA
 XX
 XX Lemieux B, Landry BS, Sapolsky RJ, Murgineux A;
 PI WPI, 1998-333252/29.
 XX
 XX Brassica species allele-specific oligonucleotide probes and primers -
 PT

useful for plant breeding.

Claim 1; Page 43; 65pp; English.

This DNA sequence is a region of a Zea mays genome which contains a polymorphic marker. This sequence can be used in the construction of allele-specific primers and probes for amplification or hybridisation, e.g. to determine common or disparate ancestry between 2 or more plants, to monitor the genetic contribution of an ancestral plant, to trace the progeny of proprietary plants, in certification of a hybrid plant or to identify the progeny of a back-crossed plant with an ancestral plant

Sequence 41 BP; 10 A; 10 C; 13 G; 8 T; 0 U; 0 Other;

Query Match 75.3%; Score 12.8; DB 2; Length 41;
Best Local Similarity 56.2%; Pred No. 1e+04; 2; Indels 0; Gaps 0;
Matches 9; Conservative 5; Mismatches 2

1 CCUGAUNUCAGUCAG 16
1 CTTGATGCAATGCG 16

RESULT 26
AAV50981
ID AAV50981 standard; DNA; 41 BP.
AAV50981;
04-JAN-1999 (first entry)

Maize polymorphic marker S43G2/G6-2B DNA.

Polymorphic marker; allele-specific; primer; probe; amplification; hybridisation; plant; hybrid certification; genetic contribution; progeny; back-cross; hybrid; ancestry; maize; ss.

Zea mays.

Key variation	Location/Qualifiers
21	
/tag= a	
/replace= g	
/note= "polymorphism"	

W09824796-A1.

11-JUN-1998.

01-DEC-1997; 97WO-US021782.

02-DEC-1996; 96US-0032069P.

07-MAR-1997; 97US-00813507.

(AFY-) AFYMETRIX INC.

Lemieux B, Landry BS, Sapolsky RJ, Murigneux A;
WPI; 1998-333252/29.

Brassica species allele-specific oligonucleotide probes and primers - useful for plant breeding.

Claim 1; Page 43; 65pp; English.

This DNA sequence is a region of a Zea mays genome which contains a polymorphic marker. This sequence can be used in the construction of allele-specific primers and probes for amplification or hybridisation, e.g. to determine common or disparate ancestry between 2 or more plants, to monitor the genetic contribution of an ancestral plant, to trace the progeny of proprietary plants, in certification of a hybrid plant or to identify the progeny of a back-crossed plant with an ancestral plant

```

SQ      Sequence 41 BP; 10 A; 10 C; 13 G; 8 T; 0 U; 0 Other;
Query Match          75.3%; Score 12.8; DB 2; Length 41;
Best Local Similarity 56.2%; Pred. No. 1e+04;
Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY      1 CCUGAUNUACAUGCAG 16
        |||::|||::|||
Db       1 CTTGATTCGATTCGAG 16

RESULT 27
AAV50994
ID      AAV50994 standard; DNA; 41 BP.
XX
XX      AAV50994;
AC
XX      04-JAN-1999 (first entry)
DT
XX
XX      Maize polymorphic marker S43G1/G3-1 DNA.
DE
XX
XX      Polymorphic marker; allele-specific; primer, probe; amplification;
KM      hybridisation; plant; hybrid certification; genetic contribution;
XX      progeny; back-cross; hybrid; ancestry; maize; ss.
OS
XX      Zea mays.
XX
XX      Key Location/Qualifiers
FH      21
FT      variation
FT      /*tag= a
FT      /replace= g
FT      /note= "polymorphism"
XX
XX      MO9824796-A1.
XX
XX      11-JUN-1998.
XX
XX      01-DEC-1997; 97WO-US021782.
XX
XX      02-DEC-1996; 96US-0032069P.
PR      07-MAR-1997; 97US-00813507.
XX
XX      (AFFY-) AFFMETRIX INC.
PA
XX      Lemieux B, Landry BS, Sapolsky RJ, Murgieux A;
PI
XX      WPI; 1998-333252/29.
DR
XX      Brassica species allele-specific oligonucleotide probes and primers -
PT      useful for plant breeding.
PT
XX      Claim 1; Page 43; 65pp; English.
PS
XX
XX      This DNA sequence is a region of a Zea mays genome which contains a
CC      polymorphic marker. This sequence can be used in the construction of
CC      allele-specific primers and probes for amplification or hybridisation,
CC      e.g. to determine common or disparate ancestry between 2 or more plants,
CC      to monitor the genetic contribution of an ancestral plant, to trace the
CC      progeny of proprietary plants, in certification of a hybrid plant or to
CC      identify the progeny of a back-crossed plant with an ancestral plant
CC
XX
SQ      Sequence 41 BP; 8 A; 9 C; 10 G; 14 T; 0 U; 0 Other;

Query Match          75.3%; Score 12.8; DB 2; Length 41;
Best Local Similarity 56.2%; Pred. No. 1e+04;
Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

OY      1 CCUGAUNUACAUGCAG 16
        |||::|||::|||
Db       1 CTTGATTCGATTCGAG 34

RESULT 28

```

AAV47798
 ID AAV47798 standard; DNA; 41 BP.
 AC AAV47798;
 XX
 XX
 DT 27-AUG-2003 (revised)
 DT 14-OCT-1998 (first entry)
 XX
 XX
 DE Maize polymorphic site oligonucleotide marker Wx1-G2/G6-2B.
 XX
 KM Maize; marker; probe; PCR primer; polymorphism; vegetal sequence;
 KM polymorphic site; corn; gramineae species; ss.
 XX
 OS Synthetic.
 OS Zea.
 XX
 PN WO9830717-A2.
 PD 16-JUL-1998.
 XX
 PF 02-DEC-1997; 97WO-EP007134.
 XX
 PR 02-DEC-1996; 96US-0032069P.
 XX
 PA (BIOC-) BIOCEM SA.
 XX
 PI Murigneux A;
 XX
 DR WPI; 1998-399160/34.
 XX
 PT Vegetal sequences including single nucleotide polymorphism - useful, e.g.
 PT to determine polymorphisms in plants; determine strain in plant breeding
 PT and to correlate polymorphisms with phenotypic traits.
 XX
 PS Claim 2; Page 13; 32pp; English.
 XX
 CC The present invention describes a nucleic acid segment comprising at
 CC least 10 contiguous nucleotides from a vegetal sequence including a
 CC polymorphic site which is a single nucleotide polymorphism (SNP), or the
 CC complement of the segment. Also described are: (1) an allele-specific
 CC oligonucleotides hybridizing to segment, or their complements, and (2) a
 CC method of analysing nucleic acids from a subject, by determining if a
 CC base is occupying any one (or a set) of polymorphic sites in 261
 CC sequences derived from six maize lines (see AAV47701 to AAV47961). The
 CC segments are useful in fingerprint analysis in plants to determine which
 CC polymorphisms are present, which strain a plant belongs to and to
 CC distinguish between strains. The polymorphisms may correlate with
 CC phenotypic traits (e.g. plant growth rate or crop yield), and the
 CC segments are useful to determine the presence/absence of specific
 CC polymorphisms correlating with the existence/absence of particular
 CC traits. The segments are also useful in marker assisted back-cross
 CC techniques to select plants with a higher percentage of recurrent parent
 CC in a back-cross population. Segments incorporate SNPs which occur more
 CC frequently than other polymorphism types and are therefore more likely to
 CC be located close to genetic loci of interest; different forms of
 CC characterised SNPs are also often easier to detect than other
 CC polymorphism types. (Updated on 27-AUG-2003 to correct OS field.)
 XX
 SQ Sequence 41 BP; 9 A; 10 C; 13 G; 8 T; 0 U; 1 Other;
 XX
 Query Match 75.3%; Score 12.8; DB 2; Length 41;
 Best Local Similarity 56.2%; Pred. No. 1e+04;
 Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
 QY 1 CCUGAUUUCAGUUGC 16
 DB 1 CTTGATTCATTCGAG 16
 1 :|||: |||:||||
 1 CTTGATTCATTCGAG 16
 RESULT 29
 AAV47809
 ID AAV47809 standard; DNA; 41 BP.
 XX

AC AAV47809;
 XX
 XX
 DT 27-AUG-2003 (revised)
 DT 14-OCT-1998 (first entry)
 XX
 XX
 DE Maize polymorphic site oligonucleotide marker Wx1-G1/G4-1.
 XX
 KM Maize; marker; probe; PCR primer; polymorphism; vegetal sequence;
 KM polymorphic site; corn; gramineae species; ss.
 XX
 OS Synthetic.
 OS Zea.
 XX
 PN WO9830717-A2.
 PD 16-JUL-1998.
 XX
 PF 02-DEC-1997; 97WO-EP007134.
 XX
 PR 02-DEC-1996; 96US-0032069P.
 XX
 PA (BIOC-) BIOCEM SA.
 XX
 PI Murigneux A;
 XX
 DR WPI; 1998-399160/34.
 XX
 PT Vegetal sequences including single nucleotide polymorphism - useful, e.g.
 PT to determine polymorphisms in plants; determine strain in plant breeding
 PT and to correlate polymorphisms with phenotypic traits.
 XX
 PS Claim 2; Page 13; 32pp; English.
 XX
 CC The present invention describes a nucleic acid segment comprising at
 CC least 10 contiguous nucleotides from a vegetal sequence including a
 CC polymorphic site which is a single nucleotide polymorphism (SNP), or the
 CC complement of the segment. Also described are: (1) an allele-specific
 CC oligonucleotides hybridizing to segment, or their complements, and (2) a
 CC method of analysing nucleic acids from a subject, by determining if a
 CC base is occupying any one (or a set) of polymorphic sites in 261
 CC sequences derived from six maize lines (see AAV47701 to AAV47961). The
 CC segments are useful in fingerprint analysis in plants to determine which
 CC polymorphisms are present, which strain a plant belongs to and to
 CC distinguish between strains. The polymorphisms may correlate with
 CC phenotypic traits (e.g. plant growth rate or crop yield), and the
 CC segments are useful to determine the presence/absence of specific
 CC polymorphisms correlating with the existence/absence of particular
 CC traits. The segments are also useful in marker assisted back-cross
 CC techniques to select plants with a higher percentage of recurrent parent
 CC in a back-cross population. Segments incorporate SNPs which occur more
 CC frequently than other polymorphism types and are therefore more likely to
 CC be located close to genetic loci of interest; different forms of
 CC characterised SNPs are also often easier to detect than other
 CC polymorphism types. (Updated on 27-AUG-2003 to correct OS field.)
 XX
 SQ Sequence 41 BP; 9 A; 10 C; 13 G; 8 T; 0 U; 1 Other;
 XX
 Query Match 75.3%; Score 12.8; DB 2; Length 41;
 Best Local Similarity 56.2%; Pred. No. 1e+04;
 Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
 QY 1 CCUGAUUUCAGUUGC 16
 DB 1 CTTGATTCATTCGAG 16
 1 :|||: |||:||||
 1 CTTGATTCATTCGAG 16
 RESULT 30
 AAV47788
 ID AAV47788 standard; DNA; 41 BP.
 XX
 AC AAV47788;
 XX
 DT 27-AUG-2003 (revised)

DT	14-OCT-1998	(first entry)	
XX			
DE	Maize polymorphic site oligonucleotide marker Wx1-G2/G6-2B.		
XX			
KW	Maize; marker; probe; PCR primer; polymorphism; vegetal sequence;		
KW	polymorphic site; corn; graminae species; ss.		
XX			
OS	Synthetic.		
OS	Zea.		
XX			
FN	W09830717-A2.		
XX			
PD	16-JUL-1998.		
XX			
PF	02-DEC-1997; 97WO-EP007134.		
XX			
PR	02-DEC-1996; 96US-0032069P.		
XX			
PA	(BIOC-) BIOCEM SA.		
XX			
PI	Mutigneux A;		
XX			
DR	WPI; 1998-399160/34.		
XX			
PT	Vegetal sequences including single nucleotide polymorphism - useful, e.g.		
PT	to determine polymorphisms in plants, determine strain in plant breeding		
PT	and to correlate polymorphisms with phenotypic traits.		
XX			
PS	Claim 2; Page 13; 32pp; English.		
XX			
CC	The present invention describes a nucleic acid segment comprising at		
CC	least 10 contiguous nucleotides from a vegetal sequence including a		
CC	polymorphic site which is a single nucleotide polymorphism (SNP), or the		
CC	complement of the segment. Also described are: (1) an allele-specific		
CC	oligonucleotides hybridising to segment, or their complements, and (2) a		
CC	method of analysing nucleic acids from a subject, by determining if a		
CC	base is occupying any one (or a set) of polymorphic sites in 261		
CC	sequences derived from six maize lines (see AA47701 to AA47961). The		
CC	segments are useful in fingerprint analysis in plants to determine which		
CC	polymorphisms are present, which strain a plant belongs to and to		
CC	distinguish between strains. The polymorphisms may correlate with		
CC	phenotypic traits (e.g. plant growth rate or crop yield), and the		
CC	segments are useful to determine the presence/absence of specific		
CC	polymorphisms correlating with the existence/absence of particular		
CC	traits. The segments are also useful in marker assisted back-cross		
CC	techniques to select plants with a higher percentage of recurrent parent		
CC	in a back-cross population. Segments incorporate SNPs which occur more		
CC	frequently than other polymorphism types and are therefore more likely to		
CC	be located close to genetic loci of interest; different forms of		
CC	characterised SNPs are also often easier to detect than other		
CC	polymorphism types. (Updated on 27-AUG-2003 to correct OS field.)		
XX			
SO	Sequence 41 BP; 9 A; 10 C; 13 G; 8 T; 0 U; 1 Other;		
XX			
Query Match	75.3%;	Score 12.8;	DB 2; Length 41;
Best Local Similarity	56.2%;	Pred. NO. 1e+04;	
Matches	9; Conservative	5; Mismatches	2; Indels 0; Gaps 0
Oy	1 CCUGAUNUCAUUGCAG 16		
	: : : :		
	: : : :		
	: : : :		
	: : : :		
Db	1 CTTGATTCATGTCAG 16		
XX			
RESULT 31			
AAH86424/C			
XX	AAH86424 standard; DNA; 63 BP.		
XX	AAH86424;		
XX			
DT	27-FEB-2002 (first entry)		
XX			
DE	Human single nucleotide polymorphism containing DNA sequence #1281.		
XX			

KW	Biallelic marker; polymorphism; human; disease; diagnosis; treatment;
KM	phenotypic trait; gene therapy; forensics; paternity; mapping; cancer;
XX	transgenic; single nucleotide polymorphism; SNP; ss.
OS	Homo sapiens.
XX	
FH	Key
FT	Location/Qualifiers
FT	variation
FT	/replace(20,C)
XX	/tag= a
XX	/standard_name="single nucleotide polymorphism"
PN	WO9953095-A2.
XX	
PD	21-OCT-1999.
XX	
PF	30-MAR-1999; 99WO-US006893.
PR	09-APR-1998; 98US-00057871.
XX	
PA	(MHED) WHITEHEAD INST BIOMEDICAL RES.
XX	
PI	Lander ES, Wang D, Hudson T;
DR	WPI; 1999-620443/53.
XX	
PT	Polymorphic human genomic sequences and related allele-specific probes
PT	and primers, useful for genetic analysis, e.g. diagnosis and monitoring
PT	of disease.
XX	
PS	Claim 1; Page 168; 330pp; English.
XX	
CC	This invention describes novel human nucleic acid segments (I) containing
CC	polymorphic sites. The polynucleotides of (I) are used for, e.g.
CC	correlating disease polymorphisms (or disease susceptibility) or other
CC	phenotypic traits (e.g. baldness, obesity, fertility, strength, response
CC	to drugs etc.); diagnosing and monitoring e.g. cancer, inflammation,
CC	heart or central nervous system diseases); detecting susceptibility to
CC	microbial infection; treating or preventing such diseases; forensic
CC	analyses; gene therapy; paternity testing; mapping genomic loci
CC	associated with phenotypic traits (and subsequent cloning of the genes
CC	responsible); and the production of transgenic organisms. Antibodies
CC	raised against (I) are useful as diagnostic and therapeutic tools and in
CC	drug screening. AAH8514 - AAH8764 represent the human DNA sequences
CC	containing biallelic polymorphic sites described in the invention
XX	
SQ	Sequence 63 BP; 18 A; 17 C; 7 G; 21 T; 0 U; 0 Other;
	Query Match 75.3%; Score 12.8; DB 2; Length 63;
	Best Local Similarity 50.0%; Pred. No. 1e+04; 2; Indels 0; Gaps 0
Matches	8; Conservative 6; Mismatches 2; Indels 0; Gaps 0
Oy	2 CUGAUNUUCAGCAGG 17
	: :: ::
	: :: ::
Db	49 CTGGTTTCATTGTAGG 34
RESULT 32	
AA127809/c	
ID	AA127809 standard; DNA; 80 BP.
AC	
XX	AA127809;
XX	
DT	12-OCT-2001 (first entry)
DE	Probe #17742 for gene expression analysis in human cervical cell sample.
XX	
KW	Probe; human; microarray; gene expression; cervical epithelial cell;
KW	cervical cancer; ss.
XX	
OS	Homo sapiens.
XX	
PN	WO200157278-A2.
XX	

PD 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US000670.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI, 2001-488901/53.
XX
DR WPI, 2001-488901/53.
XX
PS Claim 25; SEQ ID NO 17742; 487bp; English.
XX
CC The present invention relates to human single exon nucleic acid probes
CC (SENPs). The present sequence is one such probe. The SENPs are derived
CC from human HeLa cells. The SENPs can be used to produce a single exon
CC microarray, which can be used for measuring human gene expression in a
CC sample derived from human cervical epithelial cells. By measuring gene
CC expression, the probes are therefore useful in grading and/or staging of
CC diseases of the cervix, notably cervical cancer. Note: The sequence data
CC for this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 80 BP; 23 A; 25 C; 18 G; 14 T; 0 U; 0 Other;
XX
Query Match 75.3%; Score 12.8; DB 4; Length 80;
Best Local Similarity 56.2%; Pred. No. 1.1e+04;
Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
QY 2 CUGAUVUUCAGG 17
Db |||:|||||
57 CTGATTGCATTTCAGG 42
XX
RESULT 33
ABA76122/C
ID ABA76122 standard; DNA; 80 BP.
XX
XX ABA76122;
AC
XX
DT 01-FEB-2002 (first entry)
XX
XX Human foetal liver single exon nucleic acid probe #24427.
DE
XX Human; foetal liver; gene expression; single exon nucleic acid probe; ss.
KW
XX Homo sapiens.
OS
XX WO200157277-A2.
FN
XX
PD 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US000669.
PP
XX 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX

PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI, 2001-483447/52.
XX
DR WPI, 2001-483447/52.
XX
XX Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human fetal liver.
XX
XX Claim 4; SEQ ID NO 24427; 639pp + Sequence Listing; English.
XX
XX The invention relates to a single exon nucleic acid probe for measuring
CC human gene expression in a sample derived from human foetal liver. The
CC single exon nucleic acid probes may be used for predicting, measuring and
CC displaying gene expression in samples derived from human fetal liver. The
CC present sequence is a single exon nucleic acid probe of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 80 BP; 23 A; 25 C; 18 G; 14 T; 0 U; 0 Other;
XX
Query Match 75.3%; Score 12.8; DB 4; Length 80;
Best Local Similarity 56.2%; Pred. No. 1.1e+04;
Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
QY 2 CUGAUVUUCAGG 17
Db |||:|||||
57 CTGATTGCATTTCAGG 42
XX
RESULT 34
AA156782/C
ID AA156782 standard; DNA; 80 BP.
XX
XX AA156782;
AC
XX
DT 17-OCT-2001 (first entry)
XX
XX Probe #25468 used to measure gene expression in human placenta sample.
DE
XX Probe; microarray; human; placenta; antenatal diagnosis;
KW genetic disorder; ss.
XX
XX Homo sapiens.
OS
XX WO200157272-A2.
FN
XX
PD 09-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US000663.
PP
XX 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI, 2001-48897/53.
XX
DR WPI, 2001-48897/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for analyzing
PT gene expression in human placenta.
XX
XX Claim 25; SEQ ID NO 25468; 654bp; English.
XX
XX The present invention relates to single exon nucleic acid probes (SENPs).
CC The present sequence is one such probe. The probes are useful for

CC producing a microarray for predicting, measuring and displaying gene
CC expression in samples derived from human placenta. The probes are useful
CC for antenatal diagnosis of human genetic disorders

XX Sequence 80 BP; 23 A; 25 C; 18 G; 14 T; 0 U; 0 Other;

Qy Query Match 75.3%; Score 12.8; DB 4; Length 80;
Best Local Similarity 56.2%; Pred. No. 1.1e+04;
Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Oy 2 CUGAUVUUGACGAG 17
Db 57 CTGATTGCATTTCAGG 42

RESULT 35
ABA40677/C
ID ABA40677 standard; DNA; 80 BP.

XX ABA40677;

DT 23-JAN-2002 (first entry)

DE Probe #19143 for gene expression analysis in human heart cell sample.

XX Human; gene expression; heart; microarray; vascular system; probe;
KM cardiovascular disease; hypertension; cardiac arrhythmia;
KM congenital heart disease; ss.

XX Homo sapiens.

PN WO200157274-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US000666.

PR 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488899/53.

DR Single exon nucleic acid probes for analyzing gene expression in human

PT hearts.

XX Claim 4; SEQ ID NO 19143; 530pp; English.

XX The present invention relates to single exon nucleic acid probes for

CC measuring human gene expression in a sample derived from human heart. The

CC present sequence is one such probe. The probes may be used for

CC predicting, measuring and displaying gene expression in samples derived

CC from the human heart via microarrays. By measuring gene expression, the

CC probes are useful for predicting, diagnosing, grading, staging,

CC monitoring and prognosing diseases of the human heart and vascular system

CC e.g. cardiovascular disease, hypertension, cardiac arrhythmias and

CC congenital heart disease. Note: The sequence data for this patent did not

CC form part of the printed specification, but was obtained in electronic

CC format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 80 BP; 23 A; 25 C; 18 G; 14 T; 0 U; 0 Other;

Qy Query Match 75.3%; Score 12.8; DB 4; Length 80;
Best Local Similarity 56.2%; Pred. No. 1.1e+04;
Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Oy 2 CUGAUVUUGACGAG 17
Db 57 CTGATTGCATTTCAGG 42

RESULT 36
AAK50790/C
ID AAK50790 standard; DNA; 80 BP.

XX AAK50790;

DT 06-NOV-2001 (first entry)

DE Human bone marrow expressed single exon probe SEQ ID NO: 25347.

XX Human; bone marrow expressed exon; gene expression analysis; probe;
KM microarray; cancer; leukemia; lymphoma; myeloma; ss.

XX Homo sapiens.

PN WO200157276-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US000668.

PR 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488900/53.

DR Human genome-derived single exon nucleic acid probes useful for analyzing

PT gene expression in human bone marrow.

XX Example 4; SEQ ID NO 25347; 658bp + Sequence Listing; English.

PS The present invention provides a number of single exon nucleic acid

CC probes which are derived from genomic sequences expressed in the human

CC bone marrow. They can be used to measure gene expression in bone marrow

CC samples, which may enable the improved diagnosis and treatment of cancers

CC such as lymphoma, leukemia and myeloma. The present sequence is one of

CC the probes of the invention

XX Sequence 80 BP; 23 A; 25 C; 18 G; 14 T; 0 U; 0 Other;

Qy Query Match 75.3%; Score 12.8; DB 4; Length 80;
Best Local Similarity 56.2%; Pred. No. 1.1e+04;
Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Oy 2 CUGAUVUUGACGAG 17
Db 57 CTGATTGCATTTCAGG 42

RESULT 37
AAK24792/C
ID AAK24792 standard; DNA; 80 BP.

XX AAK24792;

DT 05-NOV-2001 (first entry)

DE Human brain expressed single exon probe SEQ ID NO: 24783.

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XX Human; brain expressed exon; gene expression analysis; probe; microarray;
KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;
XX ss.
OS Homo sapiens.
PN WO200157275-A2.
XX
XX 09-AUG-2001.
PD
XX 30-JAN-2001; 2001WO-US000667.
PF
XX 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-483446/52.
XX
XX Single exon nucleic acid probes for analyzing gene expression in human
XX brains.
XX
XX Example 4; SEQ ID NO 24783; 650bp + Sequence Listing; English.
XX
XX The present invention provides a number of single exon nucleic acid
XX probes which are derived from genomic sequences expressed in the human
XX brain. They can be used to measure gene expression in brain cell samples,
XX which may enable the diagnosis and improved treatment of nervous system
XX diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
XX epilepsy and cancers. The present sequence is one of the probes of the
XX invention
XX
XX Sequence 80 BP; 23 A; 25 C; 18 G; 14 T; 0 U; 0 Other;
SQ
XX
XX Query Match 75.3%; Score 12.8; DB 4; Length 80;
XX Best Local Similarity 56.2%; Pred. No. 1.1e+04;
XX Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
OY 2 CUGAUUUCAUUGCAGG 17
DB 57 CTGATTGCATTTCAGG 42

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RESULT 39
ABS50382/C
ID ABS50382 standard; DNA; 80 BP.
XX
XX ABS50382;
AC
XX
XX 25-FEB-2003 (first entry)
DT
XX
XX Human liver single exon probe, SEQ ID No 25372.
DE
XX
XX Human; single exon nucleic acid probe; liver; cirrhosis;
KW hyperlipoproteinemia; hyperlipidaemia; hypercholesterolaemia;
KW coronary heart disease; ss.
XX
XX Homo sapiens.
OS
XX
XX WO200157273-A2.
PN
XX
XX 09-AUG-2001.
PD
XX
XX 30-JAN-2001; 2001WO-US000664.
PF
XX

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PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI; 2001-488898/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for analyzing
XX gene expression in human adult liver.
XX
XX Claim 4; SEQ ID NO 25372; 658bp; English.
XX
XX The invention relates to a single exon nucleic acid probe (SENP) (I) for
XX measuring human gene expression in a sample derived from human adult
XX liver, comprising one of 1109 defined nucleotide sequences given in the
XX specification (or complements/ fragments). The probe hybridises at high
XX stringency to a nucleic acid molecule expressed in the human adult liver.
XX (I) may be used for predicting, measuring and displaying gene expression
XX in samples derived from human adult liver. The genes identified may be
XX involved in genetic liver diseases such as cirrhosis,
XX hyperlipoproteinemia, hyperlipidaemia and hypercholesterolaemia which is
XX associated with coronary heart disease. ABS25011-ABS51005 represent human
XX liver single exon nucleic acid probes of the invention. Note: The
XX sequence information for this patent does not appear in the printed
XX specification but was obtained in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 80 BP; 23 A; 25 C; 18 G; 14 T; 0 U; 0 Other;
SQ
XX
XX Query Match 75.3%; Score 12.8; DB 4; Length 80;
XX Best Local Similarity 56.2%; Pred. No. 1.1e+04;
XX Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;
OY 2 CUGAUUUCAUUGCAGG 17
DB 57 CTGATTGCATTTCAGG 42

```

```

RESULT 39
ABS24274/C
ID ABS24274 standard; DNA; 80 BP.
XX
XX ABS24274;
AC
XX
XX 19-AUG-2002 (first entry)
DT
XX
XX Human genome-derived single exon ORF from lung SEQ ID No 24265.
DE
XX
XX Human; ds; single exon probe; asthma; lung cancer; COPD; ILD;
KW chronic obstructive pulmonary disease; interstitial lung disease;
KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
KW Hereditary-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;
KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karsenger syndrome;
KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
KW primary ciliary dyskinesia; pulmonary hypertension;
KW hyaline membrane disease; open reading frame; ORF.
XX
XX Homo sapiens.
OS
XX
XX WO200186003-A2.
PN
XX
XX 15-NOV-2001.
PD
XX
XX 30-JAN-2001; 2001WO-US000665.
PF
XX

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OM nucleic - nucleic search, using sw model

Run on: May 13, 2005, 16:59:31 / Search time 42.0364 Seconds
(without alignments)
661.730 Million cell updates/sec

Title: US-09-927-046-143

Perfect score: 17

Sequence: 1 ccgaaucaucagcag 17

Scoring table: IDENTITY_NUC
Gapco 10.0, Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 1330268

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database:

Issued Patents.NA: *
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2: /cgn2_6/prodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/prodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/prodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/prodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/prodata/1/ina/Backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	13.4	78.8	25	4	US-09-396-196G-54192
C 2	13.4	78.8	25	4	US-09-396-196G-60898
C 3	13.4	78.8	25	4	US-09-396-196G-119128
C 4	12.4	72.9	20	4	US-09-422-978-9923
C 5	12.4	72.9	25	4	US-09-396-196G-3128
C 6	12.4	72.9	25	4	US-09-396-196G-3129
C 7	12.4	72.9	25	4	US-09-396-196G-27979
C 8	12.4	72.9	25	4	US-09-396-196G-105607
C 9	12.4	72.9	31	3	US-09-230-199-17
C 10	12.4	72.9	49	3	US-09-365-121-10
C 11	12.4	72.9	49	3	US-09-365-121-11
C 12	12.4	72.9	49	3	US-09-867-193-10
C 13	12.4	72.9	49	4	US-09-867-193-11
C 14	12.4	71.8	20	3	US-08-199-219-2
C 15	12.2	71.8	25	4	US-09-189-653-9
C 16	12.2	71.8	25	4	US-09-396-196G-75597
C 17	12.2	71.8	25	4	US-09-396-196G-75598
C 18	12.2	71.8	26	3	US-09-245-041-60
C 19	12.2	71.8	26	4	US-09-358-058B-61
C 20	12.2	71.8	26	4	US-09-893-238-60
C 21	12.2	71.8	30	4	US-09-426-776A-8
C 22	12.2	70.6	25	4	US-09-396-196G-108816
C 23	12.2	70.6	47	4	US-09-422-978-3740
C 24	12.2	70.6	57	4	US-09-513-999C-15276
C 25	11.8	69.4	20	3	US-09-073-567-11
C 26	11.8	69.4	20	3	US-09-073-567-34
C 27	11.8	69.4	20	3	US-09-280-805-157

28	11.8	69.4	21	2	US-08-811-492-53	Sequence 53, Appl
29	11.8	69.4	21	5	PCT-US96-10545A-53	Sequence 53, Appl
30	11.8	69.4	24	3	US-09-002-361-24	Sequence 24, Appl
31	11.8	69.4	25	2	US-08-811-492-52	Sequence 52, Appl
C 32	11.8	69.4	25	4	US-09-396-196G-22517	Sequence 22517, A
C 33	11.8	69.4	25	4	US-09-396-196G-48638	Sequence 48638, A
C 34	11.8	69.4	25	4	US-09-396-196G-88078	Sequence 88078, A
C 35	11.8	69.4	25	4	US-09-396-196G-88943	Sequence 88943, A
C 36	11.8	69.4	25	4	US-09-396-196G-88944	Sequence 88944, A
C 37	11.8	69.4	25	5	PCT-US96-10545A-52	Sequence 52, Appl
C 38	11.8	69.4	26	1	US-08-476-634-3	Sequence 3, Appl
C 39	11.8	69.4	26	1	US-08-484-518-3	Sequence 3, Appl
C 40	11.8	69.4	26	1	US-08-943-834-3	Sequence 3, Appl
C 41	11.8	69.4	51	4	US-09-443-199C-813	Sequence 813, Appl
C 42	11.8	69.4	51	4	US-09-443-199C-814	Sequence 814, Appl
C 43	11.8	69.4	65	4	US-08-956-171E-2894	Sequence 2894, Ap
C 44	11.8	69.4	65	4	US-08-781-986A-2894	Sequence 2894, Ap
C 45	11.8	69.4	68	4	US-09-313-299A-1919	Sequence 1919, Ap
C 46	11.8	69.4	84	4	US-09-513-999C-27774	Sequence 27774, A
C 47	11.8	69.4	90	4	US-09-621-976-9330	Sequence 9330, Ap
C 48	11.8	69.4	94	3	US-08-270-985-7	Sequence 7, Appl
C 49	11.8	69.4	94	3	US-08-478-208-11	Sequence 11, Appl
C 50	11.6	68.2	47	4	US-09-671-317-673	Sequence 673, Appl
C 51	11.4	67.1	19	4	US-09-696-791-263	Sequence 2693, Appl
C 52	11.4	67.1	19	4	US-09-696-791-263	Sequence 2694, Ap
C 53	11.4	67.1	22	4	US-09-548-797B-21	Sequence 21, Appl
C 54	11.4	67.1	25	4	US-09-396-196G-1653	Sequence 1653, Ap
C 55	11.4	67.1	25	4	US-09-396-196G-71293	Sequence 27979, A
C 56	11.4	67.1	25	4	US-09-396-196G-71293	Sequence 71293, A
C 57	11.4	67.1	25	4	US-09-396-196G-72224	Sequence 72224, A
C 58	11.4	67.1	25	4	US-09-396-196G-76507	Sequence 76507, A
C 59	11.4	67.1	25	4	US-09-396-196G-115075	Sequence 115075, A
C 60	11.4	67.1	25	4	US-09-396-196G-115076	Sequence 115076, A
C 61	11.4	67.1	25	4	US-09-396-196G-117033	Sequence 117033, A
C 62	11.4	67.1	25	4	US-09-396-196G-117034	Sequence 117034, A
C 63	11.4	67.1	25	4	US-09-396-196G-117035	Sequence 117035, A
C 64	11.4	67.1	25	4	US-09-396-196G-117036	Sequence 117036, A
C 65	11.4	67.1	25	4	US-09-396-196G-117037	Sequence 117037, A
C 66	11.4	67.1	25	4	US-09-396-196G-117038	Sequence 117038, A
C 67	11.4	67.1	40	1	US-08-086-428B-104	Sequence 104, Appl
C 68	11.4	67.1	40	2	US-08-468-570-104	Sequence 104, Appl
C 69	11.4	67.1	40	2	US-08-290-665A-208	Sequence 208, Appl
C 70	11.4	67.1	40	4	US-08-466-601A-104	Sequence 104, Appl
C 71	11.4	67.1	40	5	PCT-US95-10398-208	Sequence 208, Appl
C 72	11.4	67.1	73	4	US-09-513-999C-15000	Sequence 15000, A
C 73	11.4	67.1	78	3	US-09-058-483-12	Sequence 12, Appl
C 74	11.4	67.1	78	3	US-09-058-483-13	Sequence 13, Appl
C 75	11.4	67.1	78	3	US-09-058-483-14	Sequence 14, Appl
C 76	11.4	67.1	78	3	US-09-058-483-15	Sequence 15, Appl
C 77	11.4	67.1	89	4	US-09-621-976-8165	Sequence 8165, Appl
C 78	11.2	65.9	20	4	US-09-232-785-113	Sequence 113, Appl
C 79	11.2	65.9	21	4	US-09-422-978-10268	Sequence 10268, A
C 80	11.2	65.9	23	3	US-09-440-509-11	Sequence 11, Appl
C 81	11.2	65.9	23	3	US-09-153-310-30	Sequence 30, Appl
C 82	11.2	65.9	25	1	US-07-991-466-1	Sequence 1, Appl
C 83	11.2	65.9	25	1	US-08-178-660-1	Sequence 1, Appl
C 84	11.2	65.9	25	1	US-08-032-856-1	Sequence 1, Appl
C 85	11.2	65.9	25	4	US-09-396-196G-3003	Sequence 3003, Appl
C 86	11.2	65.9	25	4	US-09-396-196G-3020	Sequence 3020, Appl
C 87	11.2	65.9	25	4	US-09-396-196G-75547	Sequence 75547, A
C 88	11.2	65.9	25	4	US-09-396-196G-75547	Sequence 75547, A
C 89	11.2	65.9	25	4	US-09-396-196G-75547	Sequence 75547, A
C 90	11.2	65.9	25	4	US-09-396-196G-75547	Sequence 75547, A
C 91	11.2	65.9	25	4	US-09-396-196G-75547	Sequence 75547, A
C 92	11.2	65.9	25	4	US-09-396-196G-75547	Sequence 75547, A
C 93	11.2	65.9	25	4	US-09-396-196G-75547	Sequence 75547, A
C 94	11.2	65.9	25	4	US-09-396-196G-75547	Sequence 75547, A
C 95	11.2	65.9	25	4	US-09-396-196G-75547	Sequence 75547, A
C 96	11.2	65.9	25	4	US-09-396-196G-75547	Sequence 75547, A
C 97	11.2	65.9	25	4	US-09-396-196G-75547	Sequence 75547, A
C 98	11.2	65.9	25	4	US-09-396-196G-75547	Sequence 75547, A
C 99	11.2	65.9	25	4	US-09-396-196G-75547	Sequence 75547, A
C 100	11.2	65.9	25	4	US-09-396-196G-75547	Sequence 75547, A

ALIGNMENTS

RESULT 1

```

US-09-396-196G-54192/c
; Sequence 54192, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 54192
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-54192

```

Query Match

```

Best Local Similarity 78.8%; Score 13.4; DB 4; Length 25;
Matches 8; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      3 UGAUUUCAUUGCAG 17
       :|::||::||::||
Db      25 TCGTTTCATTGCAG 11

```

RESULT 2

```

US-09-396-196G-60898
; Sequence 60898, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60898
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-60898

```

Query Match

```

Best Local Similarity 78.8%; Score 13.4; DB 4; Length 25;
Matches 8; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      1 CCUGAUUUCAUUGCA 15
       ||::||::||::||
Db      10 CCTGATTCATTGAA 24

```

```

RESULT 3
US-09-396-196G-119128/c
; Sequence 119128, Application US/09396196G
; Patent No. 6821724

```

GENERAL INFORMATION:

```

; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 119128
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-119128

```

Query Match

```

Best Local Similarity 76.5%; Score 13; DB 4; Length 25;
Matches 7; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      3 UGAUUUCAUUGCA 15
       :|::||::||::||
Db      25 TCGATTCATTGCA 13

```

RESULT 4

```

US-09-422-978-9923/c
; Sequence 9923, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CPI
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 9923
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..20
; OTHER INFORMATION: downstream amplification primer 99-8287 for SEQ 2058, in complemer
US-09-422-978-9923

```

Query Match

```

Best Local Similarity 72.9%; Score 12.4; DB 4; Length 20;
Matches 7; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      1 CCUGAUUUCAUUGC 14
       ||::||::||::||
Db      20 CCTGATTAAATGTC 7

```

RESULT 5

```

US-09-396-196G-3128/c
; Sequence 3128, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack

```

APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3128
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-09-396-196G-3128

Query Match 72.9%; Score 12.4; DB 4; Length 25;
Best Local Similarity 57.1%; Pred. No. 2.4e+03;
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 4 GAUUCAUUGCAG 17
DB 22 GATTTCATTGTAGG 9

RESULT 6
US-09-396-196G-3129/C
Sequence 3129, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Mittleman
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3129
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-09-396-196G-3129

Query Match 72.9%; Score 12.4; DB 4; Length 25;
Best Local Similarity 57.1%; Pred. No. 2.4e+03;
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 4 GAUUCAUUGCAG 17
DB 16 GATTTCATTGTAGG 3

RESULT 7
US-09-396-196G-27979
Sequence 27979, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Mittleman
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806

SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 27979
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-09-396-196G-27979

Query Match 72.9%; Score 12.4; DB 4; Length 25;
Best Local Similarity 57.1%; Pred. No. 2.4e+03;
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 2 CUGAUUCAUUGCA 15
DB 7 CTGATTCATGCA 20

RESULT 8
US-09-396-196G-105607/C
Sequence 105607, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Mittleman
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 105607
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-09-396-196G-105607

Query Match 72.9%; Score 12.4; DB 4; Length 25;
Best Local Similarity 57.1%; Pred. No. 2.4e+03;
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 3 UGAUUCAUUGCAG 16
DB 17 TGATTTCAGTCAG 4

RESULT 9
US-09-230-199-17/C
Sequence 17, Application US/09230199
Patent No. 6294378
GENERAL INFORMATION:
APPLICANT: Houghton, Alan
APPLICANT: Bartido, Shirley M.
APPLICANT: Xu, Yigang
APPLICANT: Wang, Signu
TITLE OF INVENTION: Method and Reagents for Genetic
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSER: Oppehl & Larson
STREET: PO Box 5270
CITY: Frisco
STATE: CO
COUNTRY: USA
ZIP: 80443-5270
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS 5.0
SOFTWARE: Word Perfect
CURRENT APPLICATION DATA:

```
/ APPLICATION NUMBER: US/09/230.199
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US97/12675
/ FILING DATE: 18-JUL-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Marina T. Larson
/ REGISTRATION NUMBER: 32,038
/ REFERENCE/DOCKET NUMBER: MSK.P-012
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (970) 668-2050
/ TELEFAX: (970) 668-2082
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 17:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 31
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: genomic DNA
/ HYPOTHETICAL: no
/ ANTI-SENSE: no
/ US-09-230-199-17
```

```
Query Match 72.9%; Score 12.4; DB 3; Length 31;
Best Local Similarity 57.1%; Pred. No. 2.5e+03;
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 1 CCGAUUUCAUUGC 14
Db 24 CCTGATTCAGTCG 11
```

```
RESULT 10
US-09-365-121-10/c
/ Sequence 10, Application US/09365121
/ Patent No. 6297365
/ GENERAL INFORMATION:
/ APPLICANT: ADAMS, Christopher C.
/ APPLICANT: BRENTANO, Steven T.
/ APPLICANT: SCHROTH, Gary P.
/ TITLE OF INVENTION: DECOY PROBES
/ FILE REFERENCE: US Seq. Listing
/ CURRENT APPLICATION NUMBER: US/09/365,121
/ CURRENT FILING DATE: 1999-07-30
/ EARLIER APPLICATION NUMBER: 60/094,979
/ EARLIER FILING DATE: 1998-07-31
/ NUMBER OF SEQ ID NOS: 14
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 10
/ LENGTH: 49
/ TYPE: DNA
/ ORGANISM: synthetic construct
/ US-09-365-121-10
```

```
Query Match 72.9%; Score 12.4; DB 3; Length 49;
Best Local Similarity 57.1%; Pred. No. 2.7e+03;
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 3 UGAUUCUUAUUGCAG 16
Db 25 TGATTTCAGTCGAG 12
```

```
RESULT 11
US-09-365-121-11/c
/ Sequence 11, Application US/09365121
/ Patent No. 6297365
/ GENERAL INFORMATION:
/ APPLICANT: ADAMS, Christopher C.
/ APPLICANT: BRENTANO, Steven T.
/ APPLICANT: SCHROTH, Gary P.
```

```
/ TITLE OF INVENTION: DECOY PROBES
/ FILE REFERENCE: US Seq. Listing
/ CURRENT APPLICATION NUMBER: US/09/365,121
/ CURRENT FILING DATE: 1999-07-30
/ EARLIER APPLICATION NUMBER: 60/094,979
/ EARLIER FILING DATE: 1998-07-31
/ NUMBER OF SEQ ID NOS: 14
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 11
/ LENGTH: 49
/ TYPE: DNA
/ ORGANISM: synthetic construct
/ US-09-365-121-11
```

```
Query Match 72.9%; Score 12.4; DB 3; Length 49;
Best Local Similarity 57.1%; Pred. No. 2.7e+03;
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 3 UGAUUCUUAUUGCAG 16
Db 25 TGATTTCAGTCGAG 12
```

```
RESULT 12
US-09-867-193-10/c
/ Sequence 10, Application US/09867193
/ Patent No. 6602668
/ GENERAL INFORMATION:
/ APPLICANT: ADAMS, Christopher C.
/ APPLICANT: BRENTANO, Steven T.
/ APPLICANT: SCHROTH, Gary P.
/ TITLE OF INVENTION: DECOY PROBES
/ FILE REFERENCE: US Seq. Listing
/ CURRENT APPLICATION NUMBER: US/09/867,193
/ CURRENT FILING DATE: 2001-05-29
/ PRIOR APPLICATION NUMBER: 09/365,121
/ PRIOR FILING DATE: 1999-07-30
/ NUMBER OF SEQ ID NOS: 14
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 10
/ LENGTH: 49
/ TYPE: DNA
/ ORGANISM: synthetic construct
/ US-09-867-193-10
```

```
Query Match 72.9%; Score 12.4; DB 4; Length 49;
Best Local Similarity 57.1%; Pred. No. 2.7e+03;
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 3 UGAUUCUUAUUGCAG 16
Db 25 TGATTTCAGTCGAG 12
```

```
RESULT 13
US-09-867-193-11/c
/ Sequence 11, Application US/09867193
/ Patent No. 6602668
/ GENERAL INFORMATION:
/ APPLICANT: ADAMS, Christopher C.
/ APPLICANT: BRENTANO, Steven T.
/ APPLICANT: SCHROTH, Gary P.
/ TITLE OF INVENTION: DECOY PROBES
/ FILE REFERENCE: US Seq. Listing
/ CURRENT APPLICATION NUMBER: US/09/867,193
/ CURRENT FILING DATE: 2001-05-29
/ PRIOR APPLICATION NUMBER: 09/365,121
/ PRIOR FILING DATE: 1999-07-30
/ NUMBER OF SEQ ID NOS: 14
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 11
/ LENGTH: 49
/ TYPE: DNA
```

ORGANISM: synthetic construct
US-09-867-193-11

Query Match
Best Local Similarity 72.9%; Score 12.4; DB 4; Length 49;
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 3 UGAUUUCAGG 16
DB 25 TGATTTCAGTGCAG 12

RESULT 14
US-08-199-219-2
Sequence 2, Application US/08199219

Patent No. 6031151
Patent No. 6031151 5698768
GENERAL INFORMATION:

APPLICANT: DRAPER, JOHN
TITLE OF INVENTION: CALUS-SPECIFIC PROMOTERS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:

ADDRESSEE: HALE AND DORR
STREET: 1455 PENNSYLVANIA AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/199,219
FILING DATE: 01 MARCH 1994

PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA: APPLICATION NUMBER: PCT/GB92/01602
INFORMATION FOR SEQ ID NO: 2:
FILING DATE: 02 SEPTEMBER 1992

SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: cDNA
FEATURE:

NAME/KEY: misc.feature
LOCATION: 1..20
OTHER INFORMATION: /product= "IPCR 1 PRIMER"
US-08-199-219-2

Query Match
Best Local Similarity 71.8%; Score 12.2; DB 3; Length 20;
Matches 9; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCUGAUUUCAGG 17
DB 2 CCTGACTTATTCGCG 18

RESULT 15
US-09-189-653-9
Sequence 9, Application US/09189653

Patent No. 6171792
GENERAL INFORMATION:
APPLICANT: Brent, Roger
APPLICANT: Xu, C. Wilson

APPLICANT: Mendelsohn, Andrew R.
APPLICANT: Lok, Walter L.
TITLE OF INVENTION: DETECTION SYSTEMS FOR REGISTERING
FILE REFERENCE: 00786/317002
CURRENT APPLICATION NUMBER: US/09/189,653

CURRENT FILING DATE: 1998-11-10
EARLIER APPLICATION NUMBER: 60/065,273
EARLIER FILING DATE: 1997-11-10
NUMBER OF SEQ ID NOS: 16

SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 9
LENGTH: 25
TYPE: DNA

ORGANISM: Homo sapiens
US-09-189-653-9

Query Match
Best Local Similarity 71.8%; Score 12.2; DB 3; Length 25;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCUGAUUUCAGG 17
DB 2 CCTGACTTATTCGCG 18

RESULT 16
US-09-396-196G-75597/c
Sequence 75597, Application US/09396196G

Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Mittleman
APPLICANT: David Mack

APPLICANT: David Lockhart
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G

CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806

SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 75597
LENGTH: 25
TYPE: DNA

ORGANISM: mus musculus
US-09-396-196G-75597

Query Match
Best Local Similarity 71.8%; Score 12.2; DB 4; Length 25;
Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCUGAUUUCAGG 17
DB 23 CCTGACTTATTCGCG 7

RESULT 17
US-09-396-196G-75598/c
Sequence 75598, Application US/09396196G

Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Mittleman
APPLICANT: David Mack

APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G

CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806

SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 75598
LENGTH: 25
TYPE: DNA

ORGANISM: mus musculus

US-09-396-196G-75598

Query Match 71.8%; Score 12.2; DB 4; Length 25;
Best Local Similarity 58.8%; Pred. No. 3.1e+03;
Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCUGAUUUCAUUGCAGG 17

Db 17 CCTGATTCGATTCGAGG 1

RESULT 18
US-09-245-041-60/c

; Sequence 60, Application US/09245041
; Patent No. 6274339
; GENERAL INFORMATION:
; APPLICANT: Moore, K.
; APPLICANT: Nagle, D.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DIAGNOSIS AND TREATMENT
; FILE REFERENCE: 7853-136
; CURRENT APPLICATION NUMBER: US/09/245,041
; EARLIER FILING DATE: 1999-02-05
; EARLIER FILING DATE: 1998-07-21
; EARLIER APPLICATION NUMBER: 60/104,978
; EARLIER FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 60
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
US-09-245-041-60

Query Match 71.8%; Score 12.2; DB 3; Length 26;
Best Local Similarity 52.9%; Pred. No. 3.1e+03;
Matches 9; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCUGAUUUCAUUGCAGG 17

Db 21 CCTGATTCGATTCGAGG 5

RESULT 19

US-09-358-055B-61/c
; Sequence 61, Application US/09358055B
; Patent No. 6713277
; GENERAL INFORMATION:
; APPLICANT: Moore, K.
; APPLICANT: Nagle, D.L.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF BODY WEIGHT DISORDERS INCLUDING
; FILE REFERENCE: 7853-151
; CURRENT APPLICATION NUMBER: US/09/358,055B
; CURRENT FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: 09/245,041
; PRIOR FILING DATE: 1999-02-05
; NUMBER OF SEQ ID NOS: 153
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 61
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-358-055B-61

Query Match 71.8%; Score 12.2; DB 4; Length 26;
Best Local Similarity 52.9%; Pred. No. 3.1e+03;
Matches 9; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCUGAUUUCAUUGCAGG 17
Db 21 CCTGATTCGATTCGAGG 5

RESULT 20
US-09-893-238-60/c

; Sequence 60, Application US/09893238
; Patent No. 6727348
; GENERAL INFORMATION:
; APPLICANT: Moore, K.
; APPLICANT: Nagle, D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
; FILE REFERENCE: 7853-237
; CURRENT APPLICATION NUMBER: US/09/893,238
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: 09/245,041
; PRIOR FILING DATE: 1999-02-05
; PRIOR APPLICATION NUMBER: 60/093,630
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: 60/104,978
; PRIOR FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 60
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
US-09-893-238-60

Query Match 71.8%; Score 12.2; DB 4; Length 26;
Best Local Similarity 52.9%; Pred. No. 3.1e+03;
Matches 9; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCUGAUUUCAUUGCAGG 17

Db 21 CCTGATTCGATTCGAGG 5

RESULT 21

US-09-426-776A-8
; Sequence 8, Application US/09426776A
; Patent No. 6733997
; GENERAL INFORMATION:
; APPLICANT: DING, Jeak Ling
; APPLICANT: TAN, Ngan Soon
; APPLICANT: HO, Bow
; APPLICANT: LIM, Toong Jin
; TITLE OF INVENTION: ISOLATED NUCLEIC ACIDS ENCODING A SECRETORY SIGNAL FOR EXPRESSION
; TITLE OF INVENTION: SECRETION OF HETEROLOGOUS RECOMBINANT PROTEINS
; FILE REFERENCE: 1781-0178P
; CURRENT APPLICATION NUMBER: US/09/426,776A
; CURRENT FILING DATE: 1999-10-26
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: BamHI forward primer with BamHI restriction site and some beta-
galactosidase sequence derived from bacteria
US-09-426-776A-8

Query Match 71.8%; Score 12.2; DB 4; Length 30;
Best Local Similarity 47.1%; Pred. No. 3.2e+03;
Matches 8; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCUGAUUUCAUUGCAGG 17

Db 21 CCTGATTCGATTCGAGG 5

Db 11 CGTATTCGTTGCCG 27

RESULT 22

US-09-396-196G-108816/C
; Sequence 108816, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittlemann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 108816
; LENGTH: 25
; TYPE: DNA
; ORGANISM: mus musculus
US-09-396-196G-108816

Query Match 70.6%; Score 12; DB 4; Length 25;

Best Local Similarity 58.3%; Pred. No. 4e+03; Mismatches 0; Indels 0; Gaps 0;

Matches 7; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 6 UUCAUUGCAG 17

Db 16 TTTCATTCAG 5

RESULT 23

US-09-422-978-3740/C
; Sequence 3740, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSSET.020CPI
; CURRENT APPLICATION NUMBER: US/09/422,978
; CURRENT FILING DATE: 1999-10-20
; EARLIER APPLICATION NUMBER: US 09/298,850
; EARLIER FILING DATE: 1999-04-21
; EARLIER APPLICATION NUMBER: US 60/109,732
; EARLIER FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: US 60/082,614
; EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 3740
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 24
; OTHER INFORMATION: 99-10307-115 : polymorphic base A or G
US-09-422-978-3740

Query Match 70.6%; Score 12; DB 4; Length 47;

Best Local Similarity 50.0%; Pred. No. 4.4e+03; Mismatches 1; Indels 0; Gaps 0;

Matches 7; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 3 UCAUUCAG 16

Db 24 YGATTTCTTGCG 11

RESULT 24

US-09-513-999C-15276
; Sequence 15276, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclet, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59,US2,REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 15276
; LENGTH: 57
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-15276

Query Match 70.6%; Score 12; DB 4; Length 57;

Best Local Similarity 58.3%; Pred. No. 4.6e+03; Mismatches 0; Indels 0; Gaps 0;

Matches 7; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 6 UUCAUUGCAG 17

Db 4 TTTCATTCAG 15

RESULT 25

US-09-073-567-11/C
; Sequence 11, Application US/09073567
; Patent No. 6013786
; GENERAL INFORMATION:
; APPLICANT: Jiaodong Chen
; APPLICANT: Sudhir Agrawal
; APPLICANT: Ruiren Zhang
; TITLE OF INVENTION: MDM2-SPECIFIC ANTISENSE OLIGONUCLEOTIDES
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive, 32nd Floor
; CITY: Chicago
; STATE: IL
; COUNTRY: United States of America
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/073,567
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Greenfield, Michael S.
; REGISTRATION NUMBER: 37,147
; REFERENCE/DOCKET NUMBER: 98,057-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 913-0001
; TELEFAX: (312) 913-0002
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: linear
; MOLECULE TYPE: nucleic acid
; HYPOTHETICAL: NO

ANTI-SENSE: NO
US-09-073-567-11

Query Match
Best Local Similarity 69.4%; Score 11.8; DB 3; Length 20;
Matches 7; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 3 UGAUUCUUGCAGG 17
DB 16 TCATTTCATTCATG 2

RESULT 26

US-09-073-567-34
Sequence 34, Application US/09073567
Patent No. 6013786
GENERAL INFORMATION:
APPLICANT: Jiahdong Chen
APPLICANT: Suchir Agrawal
APPLICANT: Ruiwen Zhang
TITLE OF INVENTION: MDM2-SPECIFIC ANTISENSE OLIGONUCLEOTIDES
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive, 32nd Floor
CITY: Chicago
STATE: IL
COUNTRY: United States of America
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Microsoft Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/073,567
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Greenfield, Michael S.
REGISTRATION NUMBER: 37,147
REFERENCE/DOCKET NUMBER: 98,057-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 913-0001
TELEFAX: (312) 913-0002
INFORMATION FOR SEQ ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: nucleic acid
HYPOTHETICAL: NO
ANTI-SENSE: YES
US-09-073-567-34

Query Match
Best Local Similarity 69.4%; Score 11.8; DB 3; Length 20;
Matches 7; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 3 UGAUUCUUGCAGG 17
DB 5 TCATTTCATTCATG 19

RESULT 27

US-09-280-805-157
Sequence 157, Application US/09280805
Patent No. 6184212
GENERAL INFORMATION:
APPLICANT: Loren J. Miraglia, Pamela Nero, Mark J.
APPLICANT: Graham, Brett P. Monia
TITLE OF INVENTION: ANTISENSE MODULATION OF HUMAN MDM2

TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 271
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Jane Massey Licata
STREET: 66 East Main Street
CITY: Marlton
STATE: NJ
COUNTRY: U.S.A.

ZIP: 08053
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
COMPUTER: IBM PC
OPERATING SYSTEM: WINDOWS 95
SOFTWARE: WORDPERFECT 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/280,805
FILING DATE: herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/048,810
FILING DATE: March 26, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Licata, Jane Massey
REGISTRATION NUMBER: 32,257
REFERENCE/DOCKET NUMBER: ISPH-0346
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-810-1515
TELEFAX: 609-810-1454
INFORMATION FOR SEQ ID NO: 157:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Single
TOPOLOGY: linear
ANTI-SENSE: Yes
US-09-280-805-157

Query Match
Best Local Similarity 69.4%; Score 11.8; DB 3; Length 20;
Matches 7; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 3 UGAUUCUUGCAGG 17
DB 1 TCATTTCATTCATG 15

RESULT 28

US-08-811-492-53
Sequence 53, Application US/08811492
Patent No. 5834247
GENERAL INFORMATION:
APPLICANT: COMB, DONALD G.
APPLICANT: PERLER, FRANCINE B.
APPLICANT: JACK, WILLIAM B.
APPLICANT: XU, MING-QUN
APPLICANT: HODGES, ROBERT A.
APPLICANT: NOREN, CHRISTOPHER J.
APPLICANT: CHONG, SHAORONG S.C.
APPLICANT: ADAM, ERIC
APPLICANT: SOUTHWORTH, MAURICE
TITLE OF INVENTION: MODIFIED PROTEINS, METHODS OF THEIR
TITLE OF INVENTION: PRODUCTION AND METHODS FOR PURIFICATION OF TARGET
NUMBER OF SEQUENCES: 155
CORRESPONDENCE ADDRESS:
ADDRESSEE: GREGORY D. WILLIAMS; NEW ENGLAND BIOABS, INC.
STREET: 32 TOZER ROAD
CITY: BEVERLY
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 01915
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC\DOS\MS\ DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/811,492
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/580,555
FILING DATE: 29-DEC-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/496,247
FILING DATE: 28-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/146,885
FILING DATE: 03-NOV-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/004,139
FILING DATE: 09-DEC-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Williams, Gregory D
REGISTRATION NUMBER: 30901
REFERENCE/DOCKET NUMBER: NEB-036C4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 508-927-5054
TELEFAX: 509-927-1705
TELEX:
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-811-492-53

Query Match
Best Local Similarity 69.4%; Score 11.8; DB 2; Length 21;
Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCUGAUVUUCAGUGCA 15
Db 1 CCTGAATTCAGTGCA 15

RESULT 29
PCT-US96-10545A-53
Sequence 53, Application PC/TUS9610545A
GENERAL INFORMATION:
APPLICANT: COMB, DONALD G.
APPLICANT: PERLER, FRANTINE B.
APPLICANT: JACK, WILLIAM E.
APPLICANT: XU, MING-QUN
APPLICANT: HODGES, ROBERT A.
APPLICANT: NOREN, CHRISTOPHER J.
TITLE OF INVENTION: MODIFIED PROTEINS AND METHODS OF THEIR
TITLE OF INVENTION: PRODUCTION
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: GREGORY D. WILLIAMS; NEW ENGLAND BIOLABS, INC.
STREET: 32 TOZER ROAD
CITY: BEVERLY
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 01915
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10545A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/580,555
FILING DATE: 29-DEC-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/496,247
FILING DATE: 28-JUN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/146,885
FILING DATE: 03-NOV-1993
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/004,139
FILING DATE: 09-DEC-1992
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAMS, GREGORY D.
REGISTRATION NUMBER: 30901
REFERENCE/DOCKET NUMBER: NEB-036C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508) 927-5054
TELEFAX: (508) 927-1705
TELEX:
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
PCT-US96-10545A-53

Query Match
Best Local Similarity 69.4%; Score 11.8; DB 5; Length 21;
Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCUGAUVUUCAGUGCA 15
Db 1 CCTGAATTCAGTGCA 15

RESULT 30
US-09-002-361-24
Sequence 24, Application US/09002361
Patent No. 6329516
GENERAL INFORMATION:
APPLICANT: Halling, Blak
TITLE OF INVENTION: Lepidopteran GABA-gated chloride
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert Price & Rhoads
STREET: 997 Lenox Drive, Building 3, Suite 210
CITY: Lawrenceville
STATE: NJ
COUNTRY: USA
ZIP: 08543
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/002,361
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:

ATTORNEY/AGENT INFORMATION:
NAME: Bloom, Allen
REGISTRATION NUMBER: 29,135
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-520-3214
TELEFAX: 609-520-3259
TELEX:
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-002-361-24

Query Match 69.4%; Score 11.8; DB 3; Length 24;
Best Local Similarity 53.3%; Pred. No. 5e+03;
Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 3 UGAUUUCAUUGCAG 17
Db 5 TGAATTCATGCTGG 19

RESULT 31
US-08-811-492-52/c
Sequence 52, Application US/08811492
Patent No. 5834247
GENERAL INFORMATION:
APPLICANT: COMB, DONALD G.
APPLICANT: PERLER, FRANCINE B.
APPLICANT: JACK, WILLIAM B.
APPLICANT: XU, MING-QUN
APPLICANT: HODGES, ROBERT A.
APPLICANT: NOREN, CHRISTOPHER J.
APPLICANT: CHONG, SHARONG S.C.
APPLICANT: ADAM, ERIC
APPLICANT: SOUTHWORTH, MAURICE
TITLE OF INVENTION: MODIFIED PROTEINS, METHODS OF THEIR
TITLE OF INVENTION: PRODUCTION AND METHODS FOR PURIFICATION OF TARGET
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 155
CORRESPONDENCE ADDRESS:
ADDRESSER: GREGORY D. WILLIAMS; NEW ENGLAND BIOLABS, INC.
STREET: 32 TOZER ROAD
CITY: BEVERLY
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 01915
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC\DOS/MS\DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/811,492
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/580,555
FILING DATE: 29-DEC-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/496,247
FILING DATE: 28-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/146,885
FILING DATE: 03-NOV-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/004,139

FILING DATE: 09-DEC-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Williams, Gregory D
REGISTRATION NUMBER: 30901
REFERENCE/DOCKET NUMBER: NEB-036C4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 508-927-5054
TELEFAX: 509-927-1705
TELEX:
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-811-492-52

Query Match 69.4%; Score 11.8; DB 2; Length 25;
Best Local Similarity 60.0%; Pred. No. 5.1e+03;
Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCUGAUUUCAUUGCA 15
Db 25 CCTGATTCAGTCA 11

RESULT 32
US-09-396-196G-22517/c
Sequence 22517, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Miltmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 22517
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-09-396-196G-22517

Query Match 69.4%; Score 11.8; DB 4; Length 25;
Best Local Similarity 60.0%; Pred. No. 5.1e+03;
Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 3 UGAUUUCAUUGCAG 17
Db 20 TGATTCAGTCAGG 6

RESULT 33
US-09-396-196G-49638
Sequence 49638, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Miltmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678

```

: PRIOR FILING DATE: 1996-09-17
: NUMBER OF SEQ ID NOS: 127806
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 49638
: LENGTH: 25
: TYPE: DNA
: ORGANISM: mus musculus
US-09-396-196G-49668

```

Query Match	69.4%	Score 11.8;	DB 4;	Length 25;
Best Local Similarity	53.3%;	Pred. No. 5.1e+03;		
Matches	8;	Conservative	5;	Mismatches 2;
			Indels	0;
			Gaps	0;

```

Qy      2  CUGAUUUCAUUGCAG  16
          ||::||:|
Db      5  CTGATTTCAGTCTG  19

```

```

RESULT 34
US-09-396-196G-88078
Sequence 88078, Application US/09396196G
Patent No. 6821724
GENERAL INFORMATION:
APPLICANT: Michael Mittemann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-03-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 88078
LENGTH: 25
TYPE: DNA
ORGANISM: mus musculus
US-09-396-196G-88078

```

Query Match	69.4%	Score 11.8;	DB 4;	Length 25;
Best Local Similarity	53.3%;	Pred. No. 5.1e+03;		
Matches	8;	Conservative	5;	Mismatches 2;
			Indels	0;
			Gaps	0

Qy	3	UGA	UUC	AU	UG	CAG	17
		:	:	:	:	:	
Db	7	TCAT	CTCA	TTGC	AG	21	

```

RESULTS 35
* Sequence 89963, Application US/09396196G
* Patent No. 6621724
* GENERAL INFORMATION:
* APPLICANT: Michael Mitmann
* APPLICANT: David Mack
* APPLICANT: David Lockhart
* APPLICANT: Affymetrix, Inc.
* TITLE OF INVENTION: Methods of Genetic Analysis
* FILE REFERENCE: 3.101.1
* CURRENT FILING DATE: 1999-09-15
* PRIOR APPLICATION NUMBER: 60/100,678
* PRIOR FILING DATE: 1998-03-17
* NUMBER OF SEQ ID NOS: 127806
* SOFTWARE: FASTSEQ for Windows Version 4.0
* SEQ ID NO 89943
* LENGTH: 25
* TYPE: DNA
* ORGANISM: mus musculus
* US-09-396-196G-89943

```

Query Match	69.4%	Score 11.8	DB 4	Length 25
Best Local Similarity	46.7%	Pred. No. 5.1e+03		
Matches 7; Conservative	6;	Mismatches 2;	Indels 0;	Gaps 0;

```

QY      3 UGAUUUCAUUGCAGG 17
          :|::|::|::|
Db      21 TGGTTGATTCAGG 7

```

```

RESULT 36
Sequence 89944-196G-89944/C
Patent No. 68211724
GENERAL INFORMATION:
APPLICANT: Michael Miltmann
APPLICANT: David Mack
APPLICANT: David Lochart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/09/396,196G
CURRENT FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 89944
LENGTH: 25
TYPE: DNA
ORGANISM: mus musculus
US-09-396-196G-89944

```

Query March	69.4%	Score 11.8;	DB 4;	Length 25;
Best Local	46.7%	Pred. No. 5	1e+03;	
Matches 7;	Conservative	6;	Mismatches 2;	Indels 0;
				Gaps 0;

```

Oy      3 UGAUUCUAUUGCAGG 17
          :|::|::|::|
Db      15 TGGTTGATGCAGG 1

```

RESULT 37
PCT-US96-10545A-52/c
Sequence 52, Application PC/US9610545A
GENERAL INFORMATION:
APPLICANT: COME, DONALD G.
APPLICANT: PERLER, FRANCINE B.
APPLICANT: JACK, WILLIAM E.
APPLICANT: XU, MING-QUN
APPLICANT: HODGES, ROBERT A.
APPLICANT: NOREN, CHRISTOPHER J.
TITLE OF INVENTION: MODIFIED PROTEINS AND METHODS OF THEIR
TITLE OF INVENTION: PRODUCTION
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: GREGORY D. WILLIAMS; NEW ENGLAND BIOLABS, INC
STREET: 32 TOZER ROAD
CITY: BEVERLY
STATE: MASSACHUSETTS
COUNTRY: USA
ZIP: 01915
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentm Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10545A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/580,555
FILING DATE: 29-DEC-1995

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/496,247
FILING DATE: 28-JUN-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/146,885
FILING DATE: 03-NOV-1993
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/004,139
FILING DATE: 09-DEC-1992
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAMS, GREGORY D.
REGISTRATION NUMBER: 30901
REFERENCE/DOCKET NUMBER: NEB-036C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (508) 927-5054
TELEFAX: (508) 927-1705
TELEX:
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
PCT-US96-10545A-52

Query Match
Best Local Similarity 69.4%; Score 11.8; DB 5; Length 25;
Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCUGAUUUCAGUGCA 15
Db 25 CCTGAATTCAGTCA 11

RESULT 38
US-08-476-634-3/C
Sequence 3, Application US/08476634
Patent No. 5674995
GENERAL INFORMATION:
APPLICANT: Becherer, Kathleen Ann
APPLICANT: Dattagupta, Nanibhushan
APPLICANT: Naidu, Yathi M.
TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSER: Gen-Probe Incorporated
STREET: 9880 Campus Point Drive
CITY: San Diego
STATE: CA
COUNTRY: USA
ZIP: 92121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,634
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Fisher, Carlos A.
REGISTRATION NUMBER: 36,510
REFERENCE/DOCKET NUMBER: CB1006
TELECOMMUNICATION INFORMATION:

TELEPHONE: 619-535-2807
TELEFAX: 619-546-7929
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-476-634-3

Query Match
Best Local Similarity 69.4%; Score 11.8; DB 1; Length 26;
Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCUGAUUUCAGUGCAG 16
Db 22 CTAATTCAGTCA 8

RESULT 39
US-08-484-518-3/C
Sequence 3, Application US/08484518
Patent No. 5747470
GENERAL INFORMATION:
APPLICANT: Becherer, Kathleen
APPLICANT: Dattagupta, Nanibhushan
APPLICANT: Naidu, Yathi M.
TITLE OF INVENTION: METHOD FOR INHIBITING CELLULAR
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSER: Gen-Probe Incorporated
STREET: 9880 Campus Point Drive
CITY: San Diego
STATE: CA
COUNTRY: USA
ZIP: 92121
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,518
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Fisher, Carlos A.
REGISTRATION NUMBER: 36,510
REFERENCE/DOCKET NUMBER: CB1007
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-535-2807
TELEFAX: 619-546-7929
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-484-518-3

Query Match
Best Local Similarity 69.4%; Score 11.8; DB 1; Length 26;
Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCUGAUUUCAGUGCAG 16
Db 22 CTAATTCAGTCA 8

RESULT 40
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; Sequence 3, Application US/08943834
; Patent No. 5780612
; GENERAL INFORMATION:
; APPLICANT: Becherer, Kathleen Ann
; APPLICANT: Datagupta, Nanibhushan
; APPLICANT: Naidu, Yathi M.
; TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR
; TITLE OF INVENTION: CYTOKINE SIGNAL TRANSDUCER SP130 mRNA AS INHIBITORS OF
; TITLE OF INVENTION: DISEASE-ASSOCIATED CELLULAR PROLIFERATION
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Gen-Probe Incorporated
; STREET: 9880 Campus Point Drive
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/943,834
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/476,634
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Fisher, Carlos A.
; REGISTRATION NUMBER: 36,510
; REFERENCE/DOCKET NUMBER: CB1006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-535-2807
; TELEFAX: 619-546-7929
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-943-834-3

Query Match 69.4%; Score 11.8; DB 1; Length 26;
Best Local Similarity 53.3%; Pred. No. 5.1e+03;
Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 CUGAUUUCAUUGCAG 16
|:|::||:||||
DB 22 CTAATTCTAGTCAG 8

Search completed: May 13, 2005, 18:27:23
Job time : 45.0364 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using bw model

Run on: May 13, 2005, 16:54:55 / Search time 144.964 Seconds
(without alignments)
717.723 Million cell updates/sec

Title: US-09-927-046-143

Perfect score: 17

Sequence: 1 ccugaaucaucagcag 17

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 5662332 seqs, 3060109652 residues

Total number of hits satisfying chosen parameters: 5530346

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database:

Published Applications NA.*
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21: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	16	94.1	17	10	US-09-927-046-142
3	16	94.1	17	10	US-09-927-046-705
4	15	88.2	15	10	US-09-927-046-5413
5	15	88.2	15	10	US-09-927-046-5414
6	15	88.2	15	10	US-09-927-046-5415
7	15	88.2	15	10	US-09-927-046-141
8	15	88.2	15	9	US-09-864-761-32170
9	14.4	84.7	25	19	US-10-719-900-534802
10	14	82.4	15	10	US-09-927-046-5412
11	14	82.4	17	10	US-09-927-046-144

C 12	14	82.4	19	19	US-10-481-613-159	Sequence 159, App
C 13	14	81.2	25	19	US-10-719-900-922893	Sequence 922893,
C 14	13.8	81.2	25	19	US-10-719-900-716006	Sequence 716006,
C 15	13.4	78.8	22	14	US-10-004-2198-12	Sequence 12, Appl
C 16	13.4	78.8	22	18	US-10-787-845-12	Sequence 94994, A
C 17	13.4	78.8	25	19	US-10-719-900-94994	Sequence 94994, A
C 18	13.4	78.8	25	19	US-10-719-900-166732	Sequence 166732,
C 19	13.4	78.8	25	19	US-10-719-900-220262	Sequence 220262,
C 20	13.4	78.8	25	19	US-10-719-900-912524	Sequence 912524,
C 21	13.4	78.8	25	19	US-10-809-189-54192	Sequence 54192, A
C 22	13.4	78.8	25	19	US-10-809-189-60898	Sequence 60898, A
C 23	13.4	78.8	52	17	US-10-445-789-17	Sequence 17, Appl
C 24	13	76.5	15	10	US-09-927-046-5416	Sequence 5416, Ap
C 25	13	76.5	15	19	US-10-839-668-70	Sequence 70, Appl
C 26	13	76.5	17	10	US-09-927-046-1247	Sequence 1247, Ap
C 27	13	76.5	17	10	US-09-927-046-1671	Sequence 1671, Ap
C 28	13	76.5	25	19	US-10-719-900-36009	Sequence 36009,
C 29	13	76.5	25	19	US-10-719-900-491812	Sequence 491812,
C 30	13	76.5	25	19	US-10-719-900-813289	Sequence 813289,
C 31	13	76.5	25	19	US-10-809-189-119128	Sequence 119128,
C 32	13	76.5	43	19	US-10-741-849-1206	Sequence 1206, Ap
C 33	13	76.5	60	10	US-09-908-975-18678	Sequence 18678, A
C 34	12.8	75.3	21	18	US-10-751-736-12517	Sequence 12517, A
C 35	12.8	75.3	21	18	US-10-751-736-12518	Sequence 12518, A
C 36	12.8	75.3	21	18	US-10-098-263B-108838	Sequence 108838,
C 37	12.8	75.3	25	19	US-10-719-900-134100	Sequence 134100,
C 38	12.8	75.3	25	19	US-10-719-900-200558	Sequence 200558,
C 39	12.8	75.3	25	19	US-10-719-900-220971	Sequence 220971,
C 40	12.8	75.3	25	19	US-10-719-900-220972	Sequence 220972,
C 41	12.8	75.3	25	19	US-10-719-900-305190	Sequence 305190,
C 42	12.8	75.3	25	19	US-10-719-900-397006	Sequence 397006,
C 43	12.8	75.3	25	19	US-10-719-900-449435	Sequence 449435,
C 44	12.8	75.3	25	19	US-10-719-900-534803	Sequence 534803,
C 45	12.8	75.3	25	19	US-10-719-900-551683	Sequence 551683,
C 46	12.8	75.3	25	19	US-10-719-900-651813	Sequence 651813,
C 47	12.8	75.3	25	19	US-10-719-900-768159	Sequence 768159,
C 48	12.8	75.3	25	19	US-10-719-900-935189	Sequence 935189,
C 49	12.8	75.3	31	17	US-10-138-674-19717	Sequence 19717, A
C 50	12.8	75.3	31	18	US-10-287-949A-19717	Sequence 19717, A
C 51	12.8	75.3	31	18	US-10-712-633-5514	Sequence 5514, Ap
C 52	12.8	75.3	32	10	US-09-884-465A-173	Sequence 173, App
C 53	12.8	75.3	70	13	US-10-027-632-177723	Sequence 177723,
C 54	12.8	75.3	70	13	US-10-027-632-177740	Sequence 177740,
C 55	12.8	75.3	70	13	US-10-027-632-177757	Sequence 177757,
C 56	12.8	75.3	70	13	US-10-027-632-177773	Sequence 177773,
C 57	12.8	75.3	70	17	US-10-027-632-177723	Sequence 177723,
C 58	12.8	75.3	70	17	US-10-027-632-177740	Sequence 177740,
C 59	12.8	75.3	70	17	US-10-027-632-177757	Sequence 177757,
C 60	12.8	75.3	70	17	US-10-027-632-177774	Sequence 177774,
C 61	12.8	75.3	80	9	US-09-864-761-25997	Sequence 25997, A
C 62	12.4	72.9	20	17	US-10-349-143-9923	Sequence 9923, Ap
C 63	12.4	72.9	25	18	US-10-483-417-4	Sequence 4, Appl1
C 64	12.4	72.9	25	19	US-10-719-900-171642	Sequence 171642,
C 65	12.4	72.9	25	19	US-10-719-900-318909	Sequence 318909,
C 66	12.4	72.9	25	19	US-10-719-900-388452	Sequence 388452,
C 67	12.4	72.9	25	19	US-10-719-900-501248	Sequence 501248,
C 68	12.4	72.9	25	19	US-10-719-900-511178	Sequence 511178,
C 69	12.4	72.9	25	19	US-10-719-900-676587	Sequence 676587,
C 70	12.4	72.9	25	19	US-10-719-900-717895	Sequence 717895,
C 71	12.4	72.9	25	19	US-10-719-900-822629	Sequence 822629,
C 72	12.4	72.9	25	19	US-10-719-900-922894	Sequence 922894,
C 73	12.4	72.9	25	19	US-10-616-309-2	Sequence 2, Appl1
C 74	12.4	72.9	25	19	US-10-809-189-3128	Sequence 3128, Ap
C 75	12.4	72.9	25	19	US-10-809-189-3129	Sequence 3129, Ap
C 76	12.4	72.9	25	19	US-10-809-189-21979	Sequence 21979, A
C 77	12.4	72.9	25	19	US-10-809-189-105607	Sequence 105607,
C 78	12.4	72.9	31	9	US-09-898-541-17	Sequence 17, Appl1
C 79	12.4	72.9	49	9	US-09-867-193-10	Sequence 10, Appl1
C 80	12.4	72.9	49	9	US-09-867-193-11	Sequence 11, Appl1
C 81	12.4	72.9	49	16	US-10-375-623-10	Sequence 10, Appl1
C 82	12.4	72.9	49	16	US-10-375-623-11	Sequence 11, Appl1
C 83	12.4	72.9	60	10	US-09-908-975-7956	Sequence 7956, Ap
C 84	12.4	72.9	60	10	US-09-908-975-15199	Sequence 15199, A

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c 85 12.4 72.9 60 10 US-09-908-975-18798 Sequence 18798, A
c 86 12.4 72.9 65 15 US-09-908-975-30947 Sequence 30947, A
c 87 12.4 72.9 96 15 US-10-199-957A-52 Sequence 52, Appl
c 88 12.2 71.8 23 10 US-09-998-027-69 Sequence 69, Appl
c 89 12.2 71.8 23 16 US-10-165-099-69 Sequence 69, Appl
c 90 12.2 71.8 24 17 US-10-357-321-18 Sequence 18, Appl
c 91 12.2 71.8 25 9 US-09-757-309-9 Sequence 9, Appl
c 92 12.2 71.8 25 19 US-10-719-900-110582 Sequence 110582,
c 93 12.2 71.8 25 19 US-10-719-900-135687 Sequence 135687,
c 94 12.2 71.8 25 19 US-10-719-900-211703 Sequence 211703,
c 95 12.2 71.8 25 19 US-10-719-900-213920 Sequence 213920,
c 96 12.2 71.8 25 19 US-10-719-900-242369 Sequence 242369,
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c 98 12.2 71.8 25 19 US-10-719-900-301695 Sequence 301695,
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ALIGNMENTS

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RESULT 1
US-09-927-046-143
; Sequence 143, Application US/09927046
; Publication No. US20030064946A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc
; APPLICANT: McSwiggen, Jim
; APPLICANT: Thompson, Jim
; APPLICANT: McKenzie, Tim
; APPLICANT: Ayers, Dave
; APPLICANT: Grupe, Andrew
; APPLICANT: Szymkowski, Edmund
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chloric
; FILE REFERENCE: 249/021
; CURRENT APPLICATION NUMBER: US/09/927,046
; CURRENT FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 5450
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 143
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-927-046-143

Query Match          100.0%; Score 17; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCUGAUUUCAUUGCAGG 17
DB      1 CCUGAUUUCAUUGCAGG 17

RESULT 2
US-09-927-046-142
; Sequence 142, Application US/09927046
; Publication No. US20030064946A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc
; APPLICANT: McSwiggen, Jim
; APPLICANT: Thompson, Jim
; APPLICANT: McKenzie, Tim
; APPLICANT: Ayers, Dave
; APPLICANT: Grupe, Andrew
; APPLICANT: Szymkowski, Edmund
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chloric
; FILE REFERENCE: 249/021
; CURRENT APPLICATION NUMBER: US/09/927,046
; CURRENT FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 5450
; SOFTWARE: PatentIn version 3.0
; TYPE: DNA
; ORGANISM: Artificial Sequence

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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 142
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-927-046-142

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Query Match          94.1%; Score 16; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 CCUGAUUUCAUUGCAGG 16
DB      2 CCUGAUUUCAUUGCAGG 17

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RESULT 3
US-09-927-046-705
; Sequence 705, Application US/09927046
; Publication No. US20030064946A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc
; APPLICANT: McSwiggen, Jim
; APPLICANT: Thompson, Jim
; APPLICANT: McKenzie, Tim
; APPLICANT: Ayers, Dave
; APPLICANT: Grupe, Andrew
; APPLICANT: Szymkowski, Edmund
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chloric
; FILE REFERENCE: 249/021
; CURRENT APPLICATION NUMBER: US/09/927,046
; CURRENT FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 5450
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 705
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-927-046-705

Query Match          94.1%; Score 16; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 CCUGAUUUCAUUGCAGG 17
DB      1 CCUGAUUUCAUUGCAGG 16

RESULT 4
US-09-927-046-5413
; Sequence 5413, Application US/09927046
; Publication No. US20030064946A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc
; APPLICANT: McSwiggen, Jim
; APPLICANT: Thompson, Jim
; APPLICANT: McKenzie, Tim
; APPLICANT: Ayers, Dave
; APPLICANT: Grupe, Andrew
; APPLICANT: Szymkowski, Edmund
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chloric
; FILE REFERENCE: 249/021
; CURRENT APPLICATION NUMBER: US/09/927,046
; CURRENT FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 5450
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5413
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence

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FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-927-046-5413

Query Match 88.2%; Score 15; DB 10; Length 15;
Best Local Similarity 60.0%; Pred. No. 4.4e+02;
Matches 9; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

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|||::|::|::|::|
DB 1 CCGATTTCATTGCA 15

RESULT 5
US-09-927-046-5414

Sequence 5414, Application US/09927046
Publication No. US20030064946A1

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc

APPLICANT: MCSwigen, Jim

APPLICANT: Thompson, Jim

APPLICANT: McKenzie, Tim

APPLICANT: Ayers, Dave

APPLICANT: Grupe, Andrew

APPLICANT: Szymkowski, Edmund

TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chloric

FILE REFERENCE: 249/021

CURRENT APPLICATION NUMBER: US/09/927,046

CURRENT FILING DATE: 2001-08-09

NUMBER OF SEQ ID NOS: 5450

SOFTWARE: PatentIn version 3.0

SEQ ID NO 5414

LENGTH: 15

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-927-046-5414

Query Match 88.2%; Score 15; DB 10; Length 15;
Best Local Similarity 60.0%; Pred. No. 4.4e+02;
Matches 9; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 2 CUGAUVUUGCAG 16
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DB 1 CTGATTTCATTGCG 15

RESULT 6
US-09-927-046-5415

Sequence 5415, Application US/09927046
Publication No. US20030064946A1

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc

APPLICANT: MCSwigen, Jim

APPLICANT: Thompson, Jim

APPLICANT: McKenzie, Tim

APPLICANT: Ayers, Dave

APPLICANT: Grupe, Andrew

APPLICANT: Szymkowski, Edmund

TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chloric

FILE REFERENCE: 249/021

CURRENT APPLICATION NUMBER: US/09/927,046

CURRENT FILING DATE: 2001-08-09

NUMBER OF SEQ ID NOS: 5450

SOFTWARE: PatentIn version 3.0

SEQ ID NO 5415

LENGTH: 15

TYPE: DNA

ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-927-046-5415

Query Match 88.2%; Score 15; DB 10; Length 15;
Best Local Similarity 60.0%; Pred. No. 4.4e+02;
Matches 9; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 3 UGAUVUUGCAGG 17
:|::|::|::|::|
DB 1 TGATTTCATTGCGG 15

RESULT 7
US-09-927-046-141

Sequence 141, Application US/09927046
Publication No. US20030064946A1

GENERAL INFORMATION:

APPLICANT: Ribozyme Pharmaceuticals, Inc

APPLICANT: MCSwigen, Jim

APPLICANT: Thompson, Jim

APPLICANT: McKenzie, Tim

APPLICANT: Ayers, Dave

APPLICANT: Grupe, Andrew

APPLICANT: Szymkowski, Edmund

TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chloric

FILE REFERENCE: 249/021

CURRENT APPLICATION NUMBER: US/09/927,046

CURRENT FILING DATE: 2001-08-09

NUMBER OF SEQ ID NOS: 5450

SOFTWARE: PatentIn version 3.0

SEQ ID NO 141

LENGTH: 17

TYPE: RNA

ORGANISM: Homo sapiens
US-09-927-046-141

Query Match 88.2%; Score 15; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCUGAUVUUGCAG 15
|||::|::|::|::|
DB 3 CCUGAUVUUGCAG 17

RESULT 8
US-09-864-761-32170

Sequence 32170, Application US/09864761
Patent No. US20020048763A1

GENERAL INFORMATION:

APPLICANT: Penn, Sharon G.

APPLICANT: Rank, David R.

APPLICANT: Hanzel, David K.

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

FILE REFERENCE: Aecm1ca-X-1

CURRENT APPLICATION NUMBER: US/09/864,761

CURRENT FILING DATE: 2001-05-23

PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR FILING DATE: 2000-02-04

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: US 09/632,366

PRIOR FILING DATE: 2000-08-03

PRIOR APPLICATION NUMBER: GB 24263.6

PRIOR FILING DATE: 2000-10-04

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR FILING DATE: 2000-09-27

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00667

PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 32170
LENGTH: 88
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC010087.2
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.89
OTHER INFORMATION: SWISSPROT HIT: P38650, EVALU6.00e-03
OTHER INFORMATION: NT HIT: X95966.1, EVALU6.7.20e-01
OTHER INFORMATION: EST_HUMAN HIT: A1707484.1, EVALU6.1.70e-02
US-09-864-761-32170

Query Match 88.2%; Score 15; DB 9; Length 88;
Best Local Similarity 60.0%; Pred. No. 5.8e+02;
Matches 9; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCUGAUTCAGGCA 15
DB 63 CCTGATTCATTGCA 77

RESULT 9
US-10-719-900-534802/C
Sequence 534802, Application US/10719900
Publication No. US2005002616A1
GENERAL INFORMATION:
APPLICANT: Xue Mei Zhou
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
FILE REFERENCE: 3528.1
CURRENT APPLICATION NUMBER: US/10/719,900
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 60/427,808
PRIOR FILING DATE: 2002 11 20
NUMBER OF SEQ ID NOS: 982914
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 534802
LENGTH: 25
TYPE: DNA
ORGANISM: Mus musculus
US-10-719-900-534802

Query Match 84.7%; Score 14.4; DB 19; Length 25;
Best Local Similarity 62.5%; Pred. No. 1e+03;
Matches 10; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 2 CUGAUTCAGGCG 17
DB 22 CTGATTCATTGCG 7

RESULT 10
US-09-927-046-5412
Sequence 5412, Application US/09927046
Publication No. US20030064946A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc
APPLICANT: McSwiggen, Jim
APPLICANT: Thompson, Jim
APPLICANT: McKenzie, Tim
APPLICANT: Ayers, Dave
APPLICANT: Grupe, Andrew
TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chloric
TITLE OF INVENTION: Channel-1
FILE REFERENCE: 249/021
CURRENT APPLICATION NUMBER: US/09/927,046
CURRENT FILING DATE: 2001-08-09
NUMBER OF SEQ ID NOS: 5450
SOFTWARE: PatentIn version 3.0
SEQ ID NO 5412
LENGTH: 15
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-927-046-5412

Query Match 82.4%; Score 14; DB 10; Length 15;
Best Local Similarity 57.1%; Pred. No. 1.5e+03;
Matches 8; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCUGAUTCAGGC 14
DB 2 CCTGATTCATTGC 15

RESULT 11
US-09-927-046-144
Sequence 144, Application US/09927046
Publication No. US20030064946A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc
APPLICANT: McSwiggen, Jim
APPLICANT: Thompson, Jim
APPLICANT: McKenzie, Tim
APPLICANT: Ayers, Dave
APPLICANT: Grupe, Andrew
TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chloric
TITLE OF INVENTION: Channel-1
FILE REFERENCE: 249/021
CURRENT APPLICATION NUMBER: US/09/927,046
CURRENT FILING DATE: 2001-08-09
NUMBER OF SEQ ID NOS: 5450
SOFTWARE: PatentIn version 3.0
SEQ ID NO 144
LENGTH: 17
TYPE: RNA
ORGANISM: Homo sapiens
US-09-927-046-144

Query Match 82.4%; Score 14; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.6e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GAUUTCAGGCG 17
DB 1 GAUUTCAGGCG 14

RESULT 12

US-10-481-613-159/c
 ; Sequence 159, Application US/10481613
 ; Publication No. US20050085627A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Zhang, Youming
 ; APPLICANT: Moffatt, Miriam
 ; APPLICANT: Cookson, William
 ; APPLICANT: Tinsley, Jon
 ; TITLE OF INVENTION: Atopy
 ; FILE REFERENCE: 16721-0003US1 / P32688WO/KVC
 ; CURRENT APPLICATION NUMBER: US/10/481,613
 ; CURRENT FILING DATE: 2003-12-19
 ; PRIOR APPLICATION NUMBER: PCT/GB02/02859
 ; PRIOR FILING DATE: 2002-06-21
 ; PRIOR APPLICATION NUMBER: GB 0115211.5
 ; PRIOR FILING DATE: 2001-06-21
 ; PRIOR APPLICATION NUMBER: GB 0115212.3
 ; PRIOR FILING DATE: 2001-06-21
 ; PRIOR APPLICATION NUMBER: GB 0115213.1
 ; PRIOR FILING DATE: 2001-06-21
 ; NUMBER OF SEQ ID NOS: 326
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 159
 ; LENGTH: 19
 ; TYPE: DNA
 ; ORGANISM: Artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: Primer
 ; US-10-481-613-159

Query Match 82.4%; Score 14; DB 19; Length 19;
 Best Local Similarity 64.3%; Pred. No. 1.6e+03;
 Matches 9; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 4 GAUUCAUUCGAG 17
 ||:||||:||||
 Db 19 GATTTCATTCGAG 6

RESULT 13
 US-10-719-900-922893/c
 ; Sequence 922893, Application US/10719900
 ; Publication No. US20050026164A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xue Mei Zhou
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
 ; FILE REFERENCE: 3528.1
 ; CURRENT APPLICATION NUMBER: US/10/719,900
 ; CURRENT FILING DATE: 2003-11-20
 ; PRIOR APPLICATION NUMBER: 60/427,808
 ; PRIOR FILING DATE: 2002-11-20
 ; NUMBER OF SEQ ID NOS: 982914
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 ; SEQ ID NO 922893
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 ; US-10-719-900-922893

Query Match 82.4%; Score 14; DB 19; Length 25;
 Best Local Similarity 57.1%; Pred. No. 1.7e+03;
 Matches 8; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 3 UGAUUCAUUCGAG 16
 ||:||||:||||
 Db 21 TGATTTCATTCGAG 8

RESULT 14
 US-10-719-900-716006/c
 ; Sequence 716006, Application US/10719900
 ; Publication No. US20050026164A1
 ; GENERAL INFORMATION:

; APPLICANT: Xue Mei Zhou
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
 ; FILE REFERENCE: 3528.1
 ; CURRENT APPLICATION NUMBER: US/10/719,900
 ; CURRENT FILING DATE: 2003-11-20
 ; PRIOR APPLICATION NUMBER: 60/427,808
 ; PRIOR FILING DATE: 2002-11-20
 ; NUMBER OF SEQ ID NOS: 982914
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 ; SEQ ID NO 716006
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 ; US-10-719-900-716006

Query Match 81.2%; Score 13.8; DB 19; Length 25;
 Best Local Similarity 58.8%; Pred. No. 2.1e+03;
 Matches 10; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCUGAUUCAUUCGAG 17
 ||:||||:||||
 Db 23 CCTGATTCATTCGCGG 7

RESULT 15
 US-10-004-219B-12
 ; Sequence 12, Application US/10004219B
 ; Publication No. US20030087414A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Maciozyme
 ; APPLICANT: Aerts, Johannes M.F.G.
 ; APPLICANT: Booc, Rolf G.
 ; TITLE OF INVENTION: A mammalian mucinase, its recombinant production, and
 ; TITLE OF INVENTION: Its use in therapy or prophylaxis against diseases in
 ; TITLE OF INVENTION: which mucus is involved or infection diseases
 ; FILE REFERENCE: 2183-5136US
 ; CURRENT APPLICATION NUMBER: US/10/004,219B
 ; CURRENT FILING DATE: 2001-11-02
 ; NUMBER OF SEQ ID NOS: 14
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 12
 ; LENGTH: 22
 ; TYPE: DNA
 ; ORGANISM: Artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: primer
 ; OTHER INFORMATION: HAS3-A-tail
 ; NAME/KEY: misc feature
 ; LOCATION: (1)-(122)
 ; US-10-004-219B-12

Query Match 78.8%; Score 13.4; DB 14; Length 22;
 Best Local Similarity 53.3%; Pred. No. 3.4e+03;
 Matches 8; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 2 CUGAUUCAUUCGAG 16
 ||:||||:||||
 Db 8 CTGATTCATTCGAG 22

RESULT 16
 US-10-787-845-12
 ; Sequence 12, Application US/10787845
 ; Publication No. US20040253224A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Maciozyme
 ; APPLICANT: Aerts, Johannes M.F.G.
 ; APPLICANT: Booc, Rolf G.
 ; TITLE OF INVENTION: A mammalian mucinase, its recombinant production, and
 ; TITLE OF INVENTION: Its use in therapy or prophylaxis against diseases in
 ; TITLE OF INVENTION: which mucus is involved or infection diseases
 ; FILE REFERENCE: 2183-5136US

```
; CURRENT APPLICATION NUMBER: US/10/787,845
; CURRENT FILING DATE: 2004-02-26
; PRIOR APPLICATION NUMBER: US/10/004,219
; PRIOR FILING DATE: 2001-11-02
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 12
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
; NAME/KEY: misc.feature
; LOCATION: (1)..(22)
US-10-787-845-12

Query Match      78.8%; Score 13.4; DB 18; Length 22;
Best Local Similarity 53.3%; Pred. No. 3.4e+03;
Matches 8; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy      2 CUGAUUUCAUUGCAG 16
Db      8 CTGATTTCATTGCAG 22

RESULT 17
US-10-719-900-94994
; Sequence 94994, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 94994
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-94994

Query Match      78.8%; Score 13.4; DB 19; Length 25;
Best Local Similarity 60.0%; Pred. No. 3.5e+03;
Matches 9; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy      2 CUGAUUUCAUUGCAG 16
Db      4 CAGATTTCATTGCAG 18

RESULT 18
US-10-719-900-166732
; Sequence 166732, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 166732
; LENGTH: 25
; TYPE: DNA
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```
; ORGANISM: Mus musculus
US-10-719-900-166732

Query Match      78.8%; Score 13.4; DB 19; Length 25;
Best Local Similarity 60.0%; Pred. No. 3.5e+03;
Matches 9; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy      2 CUGAUUUCAUUGCAG 16
Db      5 CTGATTTCATTGCAG 19

RESULT 19
US-10-719-900-220262
; Sequence 220262, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 220262
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-220262

Query Match      78.8%; Score 13.4; DB 19; Length 25;
Best Local Similarity 60.0%; Pred. No. 3.5e+03;
Matches 9; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy      1 CCUGAUUUCAUUGCA 15
Db      7 CCAGATTTCATTGCA 21

RESULT 20
US-10-719-900-912524
; Sequence 912524, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 912524
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-912524

Query Match      78.8%; Score 13.4; DB 19; Length 25;
Best Local Similarity 60.0%; Pred. No. 3.5e+03;
Matches 9; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy      1 CCUGAUUUCAUUGCA 15
Db      11 CCTGATTTCATTGCA 25

RESULT 21
US-10-809-189-54192/c
; Sequence 54192, Application US/10809189
```

Publication No. US20050048531A1
GENERAL INFORMATION:
APPLICANT: Michael Wittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/10/809,189
CURRENT FILING DATE: 2004-03-25
PRIOR APPLICATION NUMBER: US/09/396,196
PRIOR FILING DATE: 1998-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 54192
LENGTH: 25
TYPE: DNA
ORGANISM: mus musculus
US-10-809-189-54192

Query Match 78.8%; Score 13.4; DB 19; Length 25;
Best Local Similarity 53.3%; Pred. No. 3.5e+03;
Matches 8; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 3 UGAUUCUAGCAGG 17
Db 25 TGCTTCATTCGACG 11

RESULT 22
US-10-809-189-60898
Sequence 60898, Application US/10809189
GENERAL INFORMATION:
APPLICANT: Michael Wittmann
APPLICANT: David Mack
APPLICANT: David Lockhart
APPLICANT: Affymetrix, Inc.
TITLE OF INVENTION: Methods of Genetic Analysis
FILE REFERENCE: 3101.1
CURRENT APPLICATION NUMBER: US/10/809,189
CURRENT FILING DATE: 2004-03-25
PRIOR APPLICATION NUMBER: US/09/396,196
PRIOR FILING DATE: 1998-09-15
PRIOR APPLICATION NUMBER: 60/100,678
PRIOR FILING DATE: 1998-09-17
NUMBER OF SEQ ID NOS: 127806
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 60898
LENGTH: 25
TYPE: DNA
ORGANISM: mus musculus
US-10-809-189-60898

Query Match 78.8%; Score 13.4; DB 19; Length 25;
Best Local Similarity 53.3%; Pred. No. 3.5e+03;
Matches 8; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCUGAUCUUCAGCA 15
Db 10 CCTGATTCATGAA 24

RESULT 23
US-10-445-789-17/c
Sequence 17, Application US/10445789
GENERAL INFORMATION:
APPLICANT: TAKESHIWA, Seiji
APPLICANT: SOGABE, Atsushi
APPLICANT: OKA, Masanori

TITLE OF INVENTION: MODIFIED PYROLOQUINOLINE QUINONE (PQQ) DEPENDENT GLUCOSE
TITLE OF INVENTION: DEHYDROGENASE WITH SUPERIOR SUBSTRATE SPECIFICITY AND STABILITY
FILE REFERENCE: 222927
CURRENT APPLICATION NUMBER: US/10/445,789
CURRENT FILING DATE: 2003-05-27
PRIOR APPLICATION NUMBER: JP 2002-152911
PRIOR FILING DATE: 2002-05-27
PRIOR APPLICATION NUMBER: JP 2002-152913
PRIOR FILING DATE: 2002-05-27
PRIOR APPLICATION NUMBER: JP 2003-080244
PRIOR FILING DATE: 2003-03-24
PRIOR APPLICATION NUMBER: JP 2003-080310
PRIOR FILING DATE: 2003-03-24
NUMBER OF SEQ ID NOS: 68
SOFTWARE: PatentIn version 3.2
SEQ ID NO 17
LENGTH: 52
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
NAME/KEY: misc_feature
LOCATION: (18)..(26)
OTHER INFORMATION: page 43, line 2 from the bottom
US-10-445-789-17

Query Match 78.8%; Score 13.4; DB 17; Length 52;
Best Local Similarity 53.3%; Pred. No. 3.9e+03;
Matches 8; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 3 UGAUUCUAGCAGG 17
Db 15 TGATTTGATTCGACG 1

RESULT 24
US-09-927-046-5416
Sequence 5416, Application US/09927046
Publication No. US20030064946A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc
APPLICANT: McSwiggen, Jim
APPLICANT: Thompson, Jim
APPLICANT: McKenzie, Tim
APPLICANT: Ayers, Dave
APPLICANT: Grupe, Andrew
APPLICANT: Szymkowski, Edmund
TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chloric
FILE REFERENCE: 249/021
CURRENT APPLICATION NUMBER: US/09/927,046
CURRENT FILING DATE: 2001-08-09
NUMBER OF SEQ ID NOS: 5450
SOFTWARE: PatentIn version 3.0
SEQ ID NO 5416
LENGTH: 15
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-927-046-5416

Query Match 76.5%; Score 13; DB 10; Length 15;
Best Local Similarity 61.5%; Pred. No. 5.3e+03;
Matches 8; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AUUCUAGCAGG 17
Db 1 ATTTCATTCGACG 13

RESULT 25

US-10-839-688-70/c
; Sequence 70, Application US/10839688
; Publication No. US20050014173A1
; GENERAL INFORMATION:
; APPLICANT: Farter, Matthew J.
; TITLE OF INVENTION: PARKINSON'S DISEASE MARKERS
; FILE REFERENCE: 07039-448001
; CURRENT APPLICATION NUMBER: US/10/839,688
; CURRENT FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: US 60/468,832
; PRIOR FILING DATE: 2003-05-08
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 70
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-839-688-70

Query Match 76.5%; Score 13; DB 19; Length 15;
Best Local Similarity 46.7%; Pred. No. 5.3e+03;
Matches 7; Conservative 7; Mismatches 1; Indels 0; Gaps 0;

QY 3 UGAUUCAUUGCAGG 17
: |||:|||||
Db 15 TTATTCTTTCGAGG 1

RESULT 26
US-09-927-046-1247
; Sequence 1247, Application US/09927046
; Publication No. US20030064946A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc
; APPLICANT: McSwiggen, Jim
; APPLICANT: Thompson, Jim
; APPLICANT: Mckenzie, Tim
; APPLICANT: Ayers, Dave
; APPLICANT: Grupe, Andrew
; APPLICANT: Szymkowski, Edmund
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chlori
; FILE REFERENCE: 249/021
; CURRENT APPLICATION NUMBER: US/09/927,046
; CURRENT FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 5450
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1247
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-927-046-1247

Query Match 76.5%; Score 13; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.4e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 AUUUCAUUGCAGG 17
: |||:|||||
Db 1 AUUUCAUUGCAGG 13

RESULT 27
US-09-927-046-1671
; Sequence 1671, Application US/09927046
; Publication No. US20030064946A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc
; APPLICANT: McSwiggen, Jim
; APPLICANT: Thompson, Jim
; APPLICANT: Mckenzie, Tim
; APPLICANT: Ayers, Dave
; APPLICANT: Grupe, Andrew

; APPLICANT: Szymkowski, Edmund
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chloric
; FILE REFERENCE: 249/021
; CURRENT APPLICATION NUMBER: US/09/927,046
; CURRENT FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 5450
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1671
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-927-046-1671

Query Match 76.5%; Score 13; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.4e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCUGAUUUCAUUG 13
: |||:|||||
Db 5 CCUGAUUUCAUUG 17

RESULT 28
US-10-719-900-360099
; Sequence 360099, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 360099
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-360099

Query Match 76.5%; Score 13; DB 19; Length 25;
Best Local Similarity 53.8%; Pred. No. 5.7e+03;
Matches 7; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 2 CUGAUUUCAUUGC 14
: |||:|||||
Db 11 CTGATTCATTGC 23

RESULT 29
US-10-719-900-491812
; Sequence 491812, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 491812
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-491812

Query Match 76.5%; Score 13; DB 19; Length 25;

Best Local Similarity 53.8%; Pred. No. 5.7e+03;
Matches 7; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 2 CCUGAUVUUGC 14
DB 10 CCGATTTCATTG 22

RESULT 30

US-10-719-900-813289
; Sequence 813289, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; NUMBER OF SEQ ID NOS: 11 20
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 813289
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-813289

Query Match 76.5%; Score 13; DB 19; Length 25;
Best Local Similarity 53.8%; Pred. No. 5.7e+03;
Matches 7; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCUGAUVUUGC 13
DB 12 CCGATTTCATTG 24

RESULT 31

US-10-809-189-119128/c
; Sequence 119128, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Mitternann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; PRIOR FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 119128
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-809-189-119128

Query Match 76.5%; Score 13; DB 19; Length 25;
Best Local Similarity 53.8%; Pred. No. 5.7e+03;
Matches 7; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 3 UGAUUCAUUGCA 15
DB 25 TGAATTCATTGCA 13

RESULT 32
US-10-741-849-1206/c

; Sequence 1206, Application US/10741849
; Publication No. US20050019931A1
; GENERAL INFORMATION:
; APPLICANT: Roemer, Terry
; APPLICANT: Jiang, Bo
; APPLICANT: Boone, Charles
; APPLICANT: Bussey, Howard
; TITLE OF INVENTION: Nucleic Acids Encoding Anti-fungal Drug Targets and Methods of

; FILE REFERENCE: 10182-023-999
; CURRENT APPLICATION NUMBER: US/10/741,849
; PRIOR FILING DATE: 2003-12-19
; PRIOR APPLICATION NUMBER: US 60/434,832
; PRIOR FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 8000
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1206
; LENGTH: 43
; TYPE: DNA
; ORGANISM: Candida albicans
US-10-741-849-1206

Query Match 76.5%; Score 13; DB 19; Length 43;
Best Local Similarity 53.8%; Pred. No. 6.2e+03;
Matches 7; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCUGAUVUUGC 13
DB 22 CCGATTTCATTG 10

RESULT 33

US-09-908-975-18678
; Sequence 18678, Application US/09908975
; Publication No. US20030165843A1
; GENERAL INFORMATION:
; APPLICANT: SHOSHAN, Avi
; APPLICANT: WASERMAN, Alon
; APPLICANT: MINTZ, Eli
; APPLICANT: MINTZ, Liat
; APPLICANT: FRIGHER, Simchon
; TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICING
; FILE REFERENCE: 36688-0005
; CURRENT APPLICATION NUMBER: US/09/908,975
; PRIOR FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/287,724
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/221,607
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 32337
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 18678
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-908-975-18678

Query Match 76.5%; Score 13; DB 10; Length 60;
Best Local Similarity 61.5%; Pred. No. 6.5e+03;
Matches 8; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 4 GAUUCAUUGCAG 16
DB 30 GAATTCATTGCG 42

RESULT 34
US-10-751-736-12517/c
; Sequence 12517, Application US/10751736
; Publication No. US20040265230A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth

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; APPLICANT: Martinez, Robert
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
; FILE REFERENCE: AM100927 (031896-002000)
; CURRENT APPLICATION NUMBER: US/10/751,736
; PRIOR FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
; NUMBER OF SEQ ID NOS: 54873
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12517
; LENGTH: 21
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-751-736-12517

Query Match
Best Local Similarity 75.3%; Score 12.8; DB 18; Length 21;
Matches 8; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Oy 2 CUGAUVUUCAUUGCAGG 17
Db 18 CTGATTCCTTGTAAG 3

RESULT 35
US-10-751-736-12518/c
; Sequence 12518, Application US/10751736
; Publication No. US20040265230A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Martinez, Robert
; APPLICANT: Brown, Eugene
; APPLICANT: Liu, Wei
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
; FILE REFERENCE: AM100927 (031896-002000)
; CURRENT APPLICATION NUMBER: US/10/751,736
; PRIOR FILING DATE: 2003-01-06
; PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
; NUMBER OF SEQ ID NOS: 54873
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12518
; LENGTH: 21
; TYPE: RNA
; ORGANISM: RNAi
US-10-751-736-12518

Query Match
Best Local Similarity 75.3%; Score 12.8; DB 18; Length 21;
Matches 8; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Oy 2 CUGAUVUUCAUUGCAGG 17
Db 16 CTGATTCCTTGTAAG 1

RESULT 36
US-10-098-263B-108838
; Sequence 108838, Application US/10098263B
; Publication No. US20030104410A1
; GENERAL INFORMATION:
; APPLICANT: Miltman, Michael
; TITLE OF INVENTION: Human Microarray
; FILE REFERENCE: 3118.1
; CURRENT APPLICATION NUMBER: US/10/098,263B
; PRIOR FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: 60/276,759
; PRIOR FILING DATE: 2001-03-16
; NUMBER OF SEQ ID NOS: 131066
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; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 108838
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-098-263B-108838

Query Match
Best Local Similarity 75.3%; Score 12.8; DB 15; Length 25;
Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Oy 1 CCUGAUVUUCAUUGCAG 16
Db 9 CCAGATTCATTGAAG 24

RESULT 37
US-10-719-900-134100/c
; Sequence 134100, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 134100
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-134100

Query Match
Best Local Similarity 75.3%; Score 12.8; DB 19; Length 25;
Matches 8; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Oy 1 CCUGAUVUUCAUUGCAG 16
Db 17 CCGAATTCCTTGTAAG 2

RESULT 38
US-10-719-900-200558
; Sequence 200558, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; PRIOR FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 200558
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-200558

Query Match
Best Local Similarity 75.3%; Score 12.8; DB 19; Length 25;
Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Oy 2 CUGAUVUUCAUUGCAG 17
Db 7 CTGATTCCTTGTAAG 22
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RESULT 39
 US-10-719-900-220971
 ; Sequence 220971, Application US/10719900
 ; Publication No. US20050026164A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xue Mei Zhou
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
 ; FILE REFERENCE: 3528.1
 ; CURRENT APPLICATION NUMBER: US/10/719,900
 ; CURRENT FILING DATE: 2003-11-20
 ; PRIOR APPLICATION NUMBER: 60/427,808
 ; PRIOR FILING DATE: 2002-11-20
 ; NUMBER OF SEQ ID NOS: 982914
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 ; SEQ ID NO 220971
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 US-10-719-900-220971

Query Match 75.3%; Score 12.8; DB 19; Length 25;
 Best Local Similarity 50.0%; Pred. No. 7.3e+03;
 Matches 8; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCUGAUUUCAGCAG 16
 ||:|::|:|
 Db 5 CCTATTATTGCG 20

RESULT 40
 US-10-719-900-220972
 ; Sequence 220972, Application US/10719900
 ; Publication No. US20050026164A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xue Mei Zhou
 ; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
 ; FILE REFERENCE: 3528.1
 ; CURRENT APPLICATION NUMBER: US/10/719,900
 ; CURRENT FILING DATE: 2003-11-20
 ; PRIOR APPLICATION NUMBER: 60/427,808
 ; PRIOR FILING DATE: 2002-11-20
 ; NUMBER OF SEQ ID NOS: 982914
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 ; SEQ ID NO 220972
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 US-10-719-900-220972

Query Match 75.3%; Score 12.8; DB 19; Length 25;
 Best Local Similarity 50.0%; Pred. No. 7.3e+03;
 Matches 8; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCUGAUUUCAGCAG 16
 ||:|::|:|
 Db 5 CCTATTATTGCG 20

Search completed: May 13, 2005, 18:25:00
 Job time : 147.964 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 13, 2005, 16:42:23 ; Search time 827.127 Seconds
(without alignments)
782.337 Million cell updates/sec

Title: US-09-927-046-143

Perfect score: 17

Sequence: 1 ccggaucacagcagcag 17

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 675282

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

EST: *
1: gb_esc1: *
2: gb_esc2: *
3: gb_hic: *
4: gb_esc3: *
5: gb_esc4: *
6: gb_esc5: *
7: gb_esc6: *
8: gb_gsa1: *
9: gb_gsa2: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
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C 2	13.4	78.8	66 7	D20621 HUMGSO1596
C 3	13.4	78.8	87 7	CO900072 Mdbb5020f
C 4	13.4	78.8	93 9	DR15E15T
C 5	13.4	78.8	94 1	AI604455 mu20h07.Y
C 6	13.4	78.8	97 7	CK098392 A013P34.5
C 7	13.4	78.8	82 2	BF506915 116P-26
C 8	12.8	75.3	52 2	BE317163 NF069A05L
C 9	12.8	75.3	60 2	BE249419 NF019A03L
C 10	12.8	75.3	61 7	CN866036 0009072AL
C 11	12.8	75.3	69 1	AA816117 VP56h06.r
C 12	12.8	75.3	71 9	CR170276 ReverseB.r
C 13	12.8	75.3	75 8	CC459199 SALK_1261
C 14	12.8	75.3	77 2	BE316157 NF029F07L
C 15	12.8	75.3	85 1	AL847774 AL847774
C 16	12.8	75.3	88 7	CK108729 1064P85.P
C 17	12.8	75.3	89 1	AA616611 VO13B01.r
C 18	12.8	75.3	89 9	CG721352 1119066E1
C 19	12.4	72.9	40 1	AA948148 on51F04.s
C 20	12.4	72.9	50 8	BZ594604 SALK_0845
C 21	12.4	72.9	54 1	AA760149 vY70D11.r
C 22	12.4	72.9	61 8	AZ762535 1M0557G06
C 23	12.4	72.9	61 8	CL528748 ASV7F11.F
C 24	12.4	72.9	63 8	BH866175 SALK_1008

C 25	12.4	72.9	65 9	CR769964 Arabidops
C 26	12.4	72.9	65 9	CG606249 OST283929
C 27	12.4	72.9	67 1	AL853876 AL853876
C 28	12.4	72.9	74 4	BM514574 KY05D03.Y
C 29	12.4	72.9	74 8	AZ468373 1M0281A22
C 30	12.4	72.9	77 8	BZ593321 SALK_0700
C 31	12.4	72.9	79 2	AM672652 1X-Exp1an
C 32	12.4	72.9	80 5	B0925856 sae83a10.
C 33	12.4	72.9	81 8	AZ339200 1M0070M06
C 34	12.4	72.9	82 8	BZ587139 3590.1.10
C 35	12.4	72.9	83 7	CN855612 000721AAA
C 36	12.4	72.9	83 8	BH791364 SALK_0598
C 37	12.4	72.9	91 8	AZ820505 2M052P06
C 38	12.4	72.9	96 6	CV2966295 EST884672
C 39	12.4	72.9	96 7	B1090229 602857182
C 40	12.4	72.9	98 4	CF035704 OCG21C02.
C 41	12.4	72.9	100 6	CF035704 OCG21C02.
C 42	12.2	71.8	52 9	CR178995 ReverseB.r
C 43	12.2	71.8	57 9	CG720057 1119060D1
C 44	12.2	71.8	57 1	AA237647 mx28g09.r
C 45	12.2	71.8	67 7	CF974344 PSU_np11\
C 46	12.2	71.8	68 9	AJ588170 Arabidops
C 47	12.2	71.8	71 7	CK106624 UB27CPB08
C 48	12.2	71.8	76 7	CK101897 F130P37.5
C 49	12.2	71.8	77 1	AI960062 BC37F04.X
C 50	12.2	71.8	77 9	CG816675 100002F18
C 51	12.2	71.8	78 1	AA197575 mu18c10.r
C 52	12.2	71.8	78 9	CG571027 CH240.446
C 53	12.2	71.8	83 9	CG522312 OST90.791
C 54	12.2	71.8	83 9	CG668947 OST465406
C 55	12.2	71.8	85 1	AA733618 AA733618
C 56	12.2	71.8	86 1	AI493964 q252D10.X
C 57	12.2	71.8	87 6	CA819137 sau69F10.
C 58	12.2	71.8	89 7	D19064 MUSGSO1271
C 59	12.2	71.8	90 2	AM059654 AHuTh.bae
C 60	12.2	71.8	91 2	AW733398 BK73803.Y
C 61	12.2	71.8	91 5	BX728604 BX728604
C 62	12.2	71.8	91 9	AL938041 Arabidops
C 63	12.2	71.8	96 9	CG615636 OST306533
C 64	12.2	71.8	97 1	AI318243 FB12C04.X
C 65	12.2	71.8	98 9	CC817050 100002F18
C 66	12.2	70.6	51 6	CB225689 1RT19G03
C 67	12.2	70.6	67 9	CN603FPL
C 68	12.2	70.6	74 9	BF642720 NF070E011
C 69	12.2	70.6	76 2	BF642720 NF070E011
C 70	12.2	70.6	77 1	AI035461 ub47c09.r
C 71	12.2	70.6	85 8	BZ593006 SALK_0550
C 72	12.2	70.6	85 9	CG628190 OST359110
C 73	12.2	70.6	94 4	BM178932 BM178932
C 74	12.2	70.6	98 1	AA625055 at66F05.r
C 75	12.2	70.6	98 4	BJ064688 BJ064688
C 76	11.8	69.4	34 1	AA853682 AA853682
C 77	11.8	69.4	33 7	R88455 R88455
C 78	11.8	69.4	53 7	BM178932 BM178932
C 79	11.8	69.4	54 4	AL769433 Arabidops
C 80	11.8	69.4	56 9	AL769433 Arabidops
C 81	11.8	69.4	57 9	CR144689 Forward.s
C 82	11.8	69.4	58 7	D18271 MUSGSO0467
C 83	11.8	69.4	58 9	CR088089 Forward.s
C 84	11.8	69.4	61 8	AZ482837 1M0308B09
C 85	11.8	69.4	61 8	AI440949 ba55509.Y
C 86	11.8	69.4	64 1	AU052007 A0052007
C 87	11.8	69.4	64 9	CG634159 OST354779
C 88	11.8	69.4	65 9	CG620109 OST316815
C 89	11.8	69.4	66 8	BH613007 SALK_0336
C 90	11.8	69.4	73 9	CR074033 Forward.B
C 91	11.8	69.4	75 1	AA702075 ZT90E02.P
C 92	11.8	69.4	75 5	B0870046 Q007E08.P
C 93	11.8	69.4	76 6	CB923183 VVD093B02
C 94	11.8	69.4	76 9	CG569409 OST197477
C 95	11.8	69.4	77 9	AG193769 Pan.trog1
C 96	11.8	69.4	78 9	CG569373 OST197379
C 97	11.8	69.4	80 1	AI357487 Q001G09.X

98 11.8 69.4 80 8 CC178575 CC178575 NEX400 Ba
 C 99 11.8 69.4 81 1 AA980013 AA980013 D58 Pea
 C 100 11.8 69.4 84 1 AT719989 AT719989 aa848c11.x

ALIGNMENTS

RESULT 1
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 LOCUS E012708-024-023-E15-SP6 MP12-ADIS-024-developing root Beta vulgaris
 DEFINITION cDNA clone 024-023-E15 5-PRIME, mRNA sequence.
 ACCESSION BQ595072
 VERSION BQ595072
 KEYWORDS GI:26124655
 SOURCE EST.
 ORGANISM Beta vulgaris
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Caryophyllales; Amaranthaceae; Beta.
 1 (bases 1 to 73)
 Herrig,R.; Schulz,B.; Weishaar,B.; Hennig,S.; Steinfath,M.;
 Drungowski,M.; Stahl,D.; Wruick,W.; Menze,A.; O'Brien,D.; Lehrach,H.
 and Radelof,U.
 Construction of a 'unigene' cDNA clone set by oligonucleotide
 fingerprinting allows access to 25 000 potential sugar beet genes
 Plant J. 32 (5), 845-857 (2002)
 22362189
 12472698

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 MEDLINE
 PUBMED
 COMMENT

ADIS DNA core facility at MP12
 Max-Planck-Institute for Plant Breeding Research
 Carl-von-Linne Weg 10, 50829 Koeln, Germany
 Fax: 00492215062851
 Email: weishaar@mp12-koeln.mpg.de
 Insert Length: 73 Std Error: 0.00
 Plate: 23 row: E column: 15
 Seq primer: SP6; CATACGATTGACGACACTATAG.
 Location/Qualifiers
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 /mol_type="mRNA"
 /cultivar="KMS2320 (double haploid, monogerm breeding
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 /db_xref="GABI:191784"
 /db_xref="taxon:161934"
 /clone="024-023-E15"
 /tissue_type="developing root"
 /lab_host="EMD108"
 /clone_1lb="MP12-ADIS-024-developing root"
 /note="Vector: PCMVSPORT6; Site 1: SalI; Site 2: NotI;
 cDNA library from sugar beet, library provided by KMS
 Kleinwanzlebener Saatucht AG Einbeck, Germany, contact:
 b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
 orientation:
 SP6-SalI-CCACGCGTCGCG-5prime-cDNA-polyA-CC-NotI-T7; Note:
 Sequencing granted in the context of the GABI-Beet
 project, local PI: Dr. Katharina Schneider, coordinator:
 Prof. Christian Jung; Sequence submission managed by
 RZPD/GABI-Primary database: http://gabi.rzpd.de"

ORIGIN

Query Match 84.7%; Score 14.4; DB 5; Length 73;
 Best Local Similarity 56.2%; Pred. No. 8e+03; 1; Indels 0; Gaps 0;
 Matches 9; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Oy 1 CCUGAUCUUCAGCAG 16
 ||:|::|::|::|::|
 Db 35 CCTATTTCATGCGAG 20

RESULT 2

D20621/c 66 bp mRNA linear EST 30-JUL-1996
 LOCUS HUMS01596 Human promyelocyte Homo sapiens cDNA pm0560 3',
 DEFINITION mRNA sequence.

ACCESSION D20621
 VERSION D20621.1 GI:501717
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 66)
 Okubo,K.; Fukushima,A.; Yoshii,J.; Niityama,T.; Kojima,Y.,
 Yoshinari,H.; Arimoto,J. and Matsubara,K.
 Gene expression of human promyelocytic cell line HL60 before and
 after induction of differentiation. A new application of 3'directed
 cDNA sequencing
 Unpublished (1993)

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

Contact: Okubo,K., Fukushima,A., Yoshii,J., Niityama,T., Kojima,Y.,
 Yoshinari,H., Arimoto,J. and Matsubara,K.
 Institute for Molecular and Cellular Biology
 Osaka University
 3-1 Yamada-oka, Suita, Osaka 565, Japan.
 Location/Qualifiers
 1..66
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="pm0560"
 /clone_1lb="Human promyelocyte"
 /note="Female, adult, cell_line = HL60, cell_type =
 promyelocyte."

FEATURES
 source
 ORIGIN

Query Match 78.8%; Score 13.4; DB 7; Length 66;
 Best Local Similarity 53.3%; Pred. No. 2.7e+04;
 Matches 8; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Oy 3 UGAUUCACUUGCAGG 17
 :|::|::|::|::|
 Db 54 TGATTTATTCGAGG 40

RESULT 3
 CO900072/c 87 bp mRNA linear EST 13-AUG-2004
 LOCUS Mddb5020f11.y1 Mddb Malus x domestica cDNA clone Mddb5020f11 5',
 DEFINITION mRNA sequence.

ACCESSION CO900072
 VERSION CO900072
 KEYWORDS GI:51239862
 SOURCE EST.
 ORGANISM Malus x domestica (cultivated apple)

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids I; Rosales; Rosaceae; Maloideae; Malus.
 1 (bases 1 to 87)
 Korban,S.; Vodka,L.; Liu,L.; Gasic,K.; Gonzales,O.; Hernandez,A.,
 Aldwinckle,H., Malnoy,M., Carroll,N., Goldbrough,P., Orysi,K.,
 Clifton,S., Page,D., Marra,M., Hillier,L., Martin,J., Wylie,T.,
 Dante,M., Theising,B., Bowers,Y., Gibbons,M., Ritter,E., Ronko,I.,
 Tsagarisvili,R., Kennedy,S., Waterson,R. and Wilson,R.
 Apple Functional Genomics grant - NSF 0321702
 Unpublished (2004)

Contact: Schuyler S. Korban
 Apple Functional Genomics grant - NSF 0321702
 Washington University School of Medicine
 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 Library materials provided by: Schuyler S. Korban Library
 constructed by: K. Gasic Library sequenced by: Washington

University Genome Sequencing Center
Washu EST name: aan23c06.y1
Seq primer: -40UP from Gibco.
Location/Qualifiers

FEATURES

1. 87

/organism="Mus mus domestica"
/mol_type="mRNA"
/cultivar="Goldrush"
/db_xref="taxon:3750"
/clone="Mdb5020f11"
/lab_host="DH10B ampicillin resistant"
/clone_1ib="Mdb5"

/note="Vector: pBluescript II SK (+); Site 1: NotI, Site 2: EcoRI; Total RNA was extracted separately from each stage (dormant terminal bud, dormant lateral bud, active lateral bud), using the 'pine tree' method. Poly(A)+mRNA was isolated twice from total RNA from each stage using the Oligotex Direct mRNA kit (Qiagen). mRNA was reverse transcribed into double stranded cDNA using a modified oligo18(dT) primer with an identifying tag sequence (see table below). cDNAs from different stages were pooled in equal amounts before adaptor ligation. Tag identification when sequencing from 5' end: Stage 1 (dormant terminal bud) insert 18(A)TCGTG; Stage 2 (dormant lateral bud) insert 18(A)TCGTG; Stage 3 (active lateral bud) insert 18(A)TCGTG; Tag identification when sequencing from 3' end: Stage 1 (dormant terminal bud) CACGA18(T) insert; Stage 2 (dormant lateral bud) CACGA18(T) insert; Stage 3 (active lateral bud) ACCGA18(T) insert; Double stranded cDNAs were size selected (more than 450 bp), adapted with EcoRI adaptors at both ends and then digested with NotI. The cDNAs were then directionally cloned into EcoRI-NotI digested pBS II SK(+) phagemid vector (Stratagene). Identification of adaptors and tags in 5'-end sequenced clones: <Vector>..TAACTT<End Vector><Start EcoRI adaptor>GATTCGATTCGATTCGCGG<End EcoRI adaptor><Start Insert>..AAAAAAAAAAAAAAAAAAAA<End Insert><Start Tag>TCGCA<End Tag><Start NotI site>GCGGCGCGCACCGCGG.. The total number of white colony forming units (cfu) in the primary library before amplification was 4x10⁵ cfu (colony forming units). The background of empty clones was less than 10%. Inserts ranged from 0.5 kb to 4 kb, as determined by PCR. Purified plasmid DNA from the primary library was converted to single-stranded circles and used as a template for PCR amplification using the T7 and T3 priming sites flanking the cloned cDNA inserts. The purified PCR products, representing the entire cloned cDNA population, were used as a driver for normalization. Hybridization between the single-stranded library and the PCR products was carried out for 44 h at 30C. Unhybridized single-stranded DNA circles were separated from hybridized DNA rendered partially double-stranded and electroporated into DH10B cells to generate the normalized library. The total number of clones with insert was 1x10⁶ cfu. Background of empty clones was less than 2%."

ORIGIN

Query Match 78.8%; Score 13.4; DB 7; Length 87;
Best Local Similarity 53.3%; Pred. No. 2.9e+04;
Matches 8; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 2 CUGAUCUUCAG 16
DB 46 CTGATTCATTGCGG 32

RESULT 4
LOCUS DR15E15T 93 bp DNA linear GSS 27-NOV-2002
DEFINITION Dario rerio genomic clone DKEX-15E15, genomic survey sequence.
ACCESSION AL747314
VERSION AL747314.1 GI:21343670

KEYWORDS
SOURCE
ORGANISM

GSS.
Dario rerio (zebrafish)
Dario rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Dario.

REFERENCE
AUTHORS Humphrey, S.J., Huckle, E. and Hunt, S.E.
TITLE Direct Submission
JOURNAL Submitted (06-JUN-2002) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact: humphrey@sanger.ac.uk Unpublished

This sequence was generated from the T7 end of BAC 15E15. 15E15 is part of the Dariokey BAC library created by R. Plaetk and N.V. Keygene.

Further details: http://www.sanger.ac.uk/Projects/D_rerio/.

FEATURES

source

1. 93
/organism="Dario rerio"
/mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEX-15E15"
/tissue_type="Testis"
/note="vector pindigobAC-536"

ORIGIN

Query Match 78.8%; Score 13.4; DB 9; Length 93;
Best Local Similarity 53.3%; Pred. No. 2.9e+04;
Matches 8; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 3 UGAAUCUUCAG 17
DB 40 TGATTCATTGAAG 26

RESULT 5
LOCUS A1604455 94 bp mRNA linear EST 21-APR-1999
DEFINITION mu20h07.y1 Soares_thymus_2bMT Mus musculus cDNA clone IMAGE:639997
5' mRNA sequence.

ACCESSION A1604455.1 GI:4613622
VERSION
KEYWORDS
SOURCE
ORGANISM

Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 94)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

JOURNAL
COMMENT
AUTHORS
TITLE

Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgsbbs-rc@mail.nih.gov

This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. This read has been verified (found to hit its original self in the correct orientation)
Seg primer: -40RP from Gibco
High quality sequence stop: 57.
Location/Qualifiers

FEATURES

source

1. 94
/organism="Mus musculus"
/mol_type="mRNA"
/strain="CS7BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:639997"
/sex="male"
/tissue_type="thymus"
/dev_stage="4 weeks"
/lab_host="DH10B"
/clone_1ib="Soares_thymus_2bMT"

ORIGIN

Query Match	78.8%	Score 13.4	DB 1	Length 94
Best Local Similarity	53.3%	Pred. No. 2.9e+04		
Matches	8	Conservative	6	Mismatches 1
				Indels 0
				Gaps 0

```
Qy      3 UGAUUUCAUUGCAGG 17
          |||::||:: |||
Db      50 TGATTTCATTCCAGG 64
```

RESULT 6

LOCUS CK098392 97 bp mRNA linear EST 01-DEC-2003
DEFINITION A01334.5PR Hybrid aspen library Populus tremula x Populus
tremuloides cDNA clone A013P34.5', mRNA sequence.

REFERENCE

AUTHORS

TITLE A Populus EST resource for functional genomics

COMMENT

Source

```

/organism="Populus tremula x Populus tremuloides"
/mol_type="mRNA"
/db_xref="taxon:47664"
/clone="A013p34"
/tissue_type="Cambial region"
/dev_stage="1.5 m actively growing tree"
/lab_host="E.coli"
/clone_id="Hybrid aspen plasmid library"
/notes="Vector: plasmidscript SK; Site 1: SalI; Site 2: NotI;
the Cambial region tissues, including developing xylem, the
meristematic cambial zone and the developing and mature
phloem, was harvested from 1.5 m actively growing trees.
cDNA was prepared and cloned into lambda gtc2a. DNA was
isolated and subcloned into plasmidscript SK using SalI and
NotI restriction enzymes."

```

ORIGIN

Query Match	78.8%;	Score 13.4;	DB 7;	Length 97;
Best Local Similarity	53.3%;	Pred. No. 2.9e+04;		
Matches	8;	Conservative	6;	Mismatches 1;
				Indels 0;
				Gaps 0;

QY 2 CUGAUUUCAUUGCAG 16

Db 50 CTGCTTTCATGCA 64

RESULT 7

LOCUS	BF506915	82 bp	mRNA	linear	EST 07-DEC-2000
DEFINITION	1116P-26 Pooled green leaf and root tissue Sorghum bicolor cDNA clone 1116P-26, mRNA sequence.				

REFERENCE	AUTHORS	TITLE
1 (bases 1 to 82)	Childs, K.L., Klein, R.R., Klein, P.E., Morishige, D.T. and Mullet, J.E.	Mapping Genes on an Integrated Sorghum Genetic and Physical Map

COMMENT

COMMENT

FEATURES
SOURCE

FEATURES

SOURCE

```

/organism="Sorghum bicolor"
/mol_type="mRNA"
/cultivar="BTx623"
/db_xref="taxon:4558"
/clone="116P-26"
/tissue_type="green leaf and root tissue"
/clone_1b="Pooled green leaf and root tissue"
/name="Vector: pBluescript II (SK), Site_1: EcoRI, Site_2:
SccRI"

```

ORIGIN

Query Match	76.5%	Score 13;	DB 2;	Length 82
Best Local Similarity	61.5%;	Pred. No. 4.6e+04;		
Matches	8;	Conservative	5;	Mismatches 0; Indels

RESULT 8

LOCUS	52 bp	mrna	linear	EST 21-DEC-2000
DEFINITION	Developing leaf	Medicago	truncatula	cdna clone
DESCRIPTION	NF069A05LF 5', mRNA sequence.			

REFERENCE AUTHORS

TITLE

JOURNAL

[illegible]

LOCUS	CG721352	89 bp	DNA	linear	SSS 20-OCT-2003
DEFINITION	1119066E12.y1 1119 - Rescuetm Grid AA Zea mays genomic, genomic survey sequence.				
ACCESSION	CG721352				
VERSION	CG721352.1	GI:37755139			
KEYWORDS	SSS.				
SOURCE	Zea mays				
ORGANISM	Zea mays				
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoidae; Andropogoneae; Zea.				
AUTHORS	1 (bases 1 to 89)				
TITLE	Walbot.V.				
JOURNAL	Maize genomic sequences found using engineered Rescuetm transposon Unpublished (2001)				
COMMENT	Contact: Walbot V Department of Biological Sciences Stanford University 855 California Ave, Palo Alto, CA 94304, USA Tel: 650 723 2227 Fax: 650 723 8221 Email: walbot@stanford.edu Plate: 1119066 row: B column: 12 Class: transposon-tagged. Location/Qualifiers				
FEATURES					
Source	1..89				
	/organism="Zea mays"				
	/mol_type="genomic DNA"				
	/cultivar="mixed background W23/A188/B73/K55"				
	/db_xref="taxon:4577"				
	/taeue_type="leaf"				
	/dev_stage="adult"				
	/lab_host="DH10B"				
	/clone_1b="1119 - Rescuetm Grid AA"				
	/note="Organ: leaf; Vector: Rescuetm (engineered from pBuescript backbone); Site 1: BamHI, Site 2: BglII; Rescuetm is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on Rescuetm, go to the web site 'www.zmcb.iastate.edu' and follow the links for 'Rescuetm.' Grid AA was grown at UC San Diego in 2002. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."				
ORIGIN					
Query Match	75.3%	Score 12.8;	DB 9;	Length 89;	
Best Local Similarity	56.2%;	Pred. No. 5.9e+04;			
Matches	9;	Conservative 5;	Mismatches 2;	Indels 0;	Gaps 0;
OY	2	CUGAUNUCAGUCGAG 17			
	: :: ::				
Db	34	CTGATCTTGCAGG 49			
RESULT 19	AA948148/c	40 bp	mRNA	linear	EST 23-JUN-1998
LOCUS	AA948148/c				
DEFINITION	ons1f04.81 NCI CGAP C08 Homo sapiens cDNA clone IMAGE:1560223 3'				
	similar to SW:5100_HUMAN Q16186 110 KD CELL MEMBRANE GLYCOPROTEIN.				
	;', mRNA sequence.				
ACCESSION	AA948148				
VERSION	AA948148.1	GI:3109401			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE	1 (bases 1 to 40)				
AUTHORS	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .				
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),				

JOURNAL
COMMENT

Tumor Gene Index
Unpublished (1997)
Contact: Robert Straubeberg, Ph.D.
Email: cga@rsf-mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmett-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
www.bio.linn.gov/bbrp/image/image.html

FEATURES
source

Trace considered overall poor quality
Insert Length: 1052 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 1.
Location/Qualifiers

1.40
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1560223"
/tissue_type="adenocarcinoma"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_C08"
/note="Organ: colon; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; 1st strand cDNA was prepared from
colon adenocarcinoma, and was then primed with a Not I -
oligo(dT) primer. Double-stranded cDNA was ligated to Eco
RI adaptors (Pharmacia), digested with Not I and cloned
into the Not I and Eco RI sites of the modified pT73
vector. Library is normalized. Library was constructed by
Bento Soares and M. Fatima Bonaldo."

ORIGIN

Query Match 72.9%; Score 12.4; DB 1; Length 40;
Best Local Similarity 50.0%; Pred. No. 8.6e+04;
Matches 7; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCUGAUVUCAUUGC 14
Db 40 CCGATTCAATTCG 27

RESULT 20
BZ594604/c 50 bp DNA linear GSS 07-JAN-2003
LOCUS SALK_084582.16.35.x Arabidopsis thaliana TDNA insertion lines
DEFINITION Arabidopsis thaliana genomic clone SALK_084582.16.35.x, genomic
survey sequence.

ACCESSION BZ594604
VERSION BZ594604
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (chale creas)
ORGANISM Arabidopsis thaliana

REFERENCE 1 Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadgil,N.C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shim,P., Zimmerman,J., and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)

JOURNAL TITLE
COMMENT Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu

FEATURES
source

This is single pass sequence recovered from the left border of
TDNA. This sequence lies within an annotated intron of At5g44580.
Class: TDNA tagged.
Location/Qualifiers

1.50
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_084582.16.35.x"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://sigal.salk.edu/cdna_protocols.html"

ORIGIN

Query Match 72.9%; Score 12.4; DB 8; Length 50;
Best Local Similarity 57.1%; Pred. No. 8.9e+04;
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CCUGAUVUCAUUGCA 15
Db 35 CCGATTCAATTCGA 22

RESULT 21
AA760149 54 bp mRNA linear EST 23-JAN-1998
LOCUS VV70B11.r1 StrataGene mouse skin (#937313) Mus musculus cDNA clone
DEFINITION IMAGE:1227741 5', mRNA sequence.
ACCESSION AA760149
VERSION AA760149.1 GI:2807943

KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Gaisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Stepcoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterson,R.
The WashU-HMI Mouse EST Project
Unpublished (1996)
Contact: Maria M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LINL; contact the
IMAGE Consortium (info@image.linn.gov) for further information.
MGI:653333
Seq primer: -28m13 rev1 ET from Amersham.

FEATURES
source

1.54
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:1227741"
/sex="females"
/tissue_type="whole skin"
/dev_stage="11 weeks old"
/lab_host="SOLR (kanamycin resistant)"
/clone_lib="StrataGene mouse skin (#937313)"
/note="Organ: skin; Vector: pBluescript SK-; Site 1:
Bcor1; Site 2: XhoI; Cloned unidirectionally. Primer:

Oligo dT Whole skin from 11 week old C57BL/6 female mice.
Average insert size: 1.0 kb; Uni-ZAP XR Vector; ~5'
adaptor sequence: 5' GAATTCGGACGAG 3' ~3' adaptor
sequence: 5' CTCGAGTTTTTTTTTTTTT 3' "

ORIGIN

	72.9%;	Score 12.4;	DB 1,	Length 54;
Query Match	Similarity	64.3%;	Pred.	No. 9e+04;
Best Local	Matches	9;	Mismatches	1;
			Indels	0;
			Gaps	0;
Qy	4 GAUUCACUUGCAGG	17		
	: :			
Db	38 GATTTCATGGCAGG	51		

RESULT 22	
A2762535	
LOCUS	61 bp DNA linear GSS 16-FEB-2001
DEFINITION	IN0557G06R Mouse 10kb plasmid U06C1M library Mus musculus genomic clone U06C1M0557G06 R, genomic survey sequence.

purified, sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match	72.9%	Score 12.4	DB 8	Length 61
Best Local Similarity	50.0%	Pred. No. 9	2e+04	
Matches	7	Conservative	6	Mismatches 1, Indels 0, Gaps 0;
QY	1	CCGGAUUTUCAUUGC	14	
Db	17	CCGGAATTAAATGC	30	

RESULT 23				
CL528748/c				
LOCUS	CL528748	61 bp	DNA	linear
DEFINITION	ASV7f11.fwd ASLV-vector integration sites in human 293T-TVA cells			
	Homo sapiens genomic clone ASV7f11.fwd, genomic survey sequence.			

TITLE	Mouse whole genome scaffolding with paired end reads from 10kb
JOURNAL	plasmid inserts
COMMENT	Unpublished (2000)
Contact:	Robert B. Weiss

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0557 row: G column: 06
Seq primer: CACACAGGAACGCTATGACC
Class: plasmid ends
High quality sequence stop: 61.

FEATURES

Fax: 858 554 0341
Email: bushman@salk.edu
Class: PCR with specific primers.
Location/Qualifiers

```
Location/Qualifiers
1. .61
/organism="Mus musculus"
/mol type="genomic DNA"
```

Query Match	72.9%	Score 12.4	DB 9	Length 61
Best Local Similarity	57.1%	Pred. No. 9	2E+04	
Matches	8	Conservative	1	Indels 0
		Mismatches	1	Gaps 0
QY	2	CUGAUAUUGCA	15	
	: : : : :			
Match	38	CTGACCTTCATGCA	25	

LOCUS	63 bp	DNA	linear	GSS 05-AUG-2002
BH866175				
SAHK100839	Arabidopsis thaliana	TDNA insertion lines	Arabidopsis	
DEFINITION	thaliana genomic clone SAHK100839, genomic survey sequence.			

ACCESSION BH866175
 VERSION BH866175.1 GI:22102073
 KEYWORDS GSS.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eustosids II; Brassicales; Brassicaceae; Arabidopsids.
 1 (bases 1 to 63)
 REFERENCE
 AUTHORS Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J. and Becker, J.R.
 A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
 Unpublished (2001)
 JOURNAL
 COMMENT Contact: Joseph R. Becker
 Salk Institute Genomic Analysis Laboratory (SIGAL)
 The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: ecker@salk.edu
 This is single pass sequence recovered from the left border of TDNA.
 Class: TDNA tagged.
 FEATURES
 source
 Location/Qualifiers
 1..63
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /ecotype="Col-0"
 /db_xref="taxon:3702"
 /clone_lib="SALK_100839"
 /note="PCR was performed on Arabidopsis thaliana T-DNA insertion lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match 72.9%; Score 12.4; DB 8; Length 63;
 Best Local Similarity 50.0%; Pred. No. 9.2e+04;
 Matches 7; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 2 CUGAUUUCANUGCA 15
 Db 28 CTGATTCATTGTA 15

RESULT 25
 CR769964 65 bp DNA linear GSS 15-SEP-2004
 LOCUS Arabidopsis thaliana T-DNA flanking sequence GK-032E03-027723.
 DEFINITION genomic survey sequence.
 ACCESSION CR769964
 VERSION CR769964.1 GI:52137886
 KEYWORDS GSS.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eustosids II; Brassicales; Brassicaceae; Arabidopsids.
 1 (bases 1 to 65)
 REFERENCE
 AUTHORS Li, Y., Rosso, M.G., Strizhov, N., Viehoveer, P. and Weishaar, B.
 GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana
 Bioinformatics 19 (11), 1441-1442 (2003)
 JOURNAL MEDLINE 22755829
 PUBMED 12874060
 REFERENCE
 AUTHORS Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and

TITLE Weishaar, B.
 An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics
 JOURNAL Plant Mol. Biol. 53 (1-2), 247-259 (2003)
 MEDLINE 23117147
 PUBMED 14756321
 REFERENCE
 AUTHORS Strizhov, N., Li, Y., Rosso, M.G., Viehoveer, P., Dekker, K.A. and Weishaar, B.
 High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines
 Biotechniques 35 (6), 1164-1168 (2003)
 JOURNAL MEDLINE 23044198
 PUBMED 14682050
 REFERENCE
 AUTHORS Rosso, M.G., Li, Y., Strizhov, N. and Weishaar, B.
 Direct Submission
 Submitted (15-SEP-2004) Weishaar B., Max-Planck-Institut fuer Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
 This sequence has been recovered from the left border of the T-DNA. It indicates an insertion close to or within gene AT3G51880.
 Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project.
 GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.
 FEATURES
 source
 Location/Qualifiers
 1..65
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /strain="Columbia 0"
 /db_xref="taxon:3702"
 /clone_lib="GK-032E03-027723"
 /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
 /ecotype="Col-0"
 /note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC106 (Genbank accession number: AY537513). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

ORIGIN

Query Match 72.9%; Score 12.4; DB 9; Length 65;
 Best Local Similarity 50.0%; Pred. No. 9.3e+04;
 Matches 7; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 2 CUGAUUUCANUGCA 15
 Db 52 CTGATTCCTTGCA 39

RESULT 26
 CG606249 65 bp mRNA linear GSS 02-OCT-2003
 LOCUS OSTR83929 Mus musculus 129Sv/Ev Mus musculus cDNA clone OSTR83929.
 DEFINITION mRNA sequence.
 ACCESSION CG606249
 VERSION CG606249.1 GI:37429925
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 65)
 REFERENCE
 AUTHORS Zambowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J., Piggett, C.J., Beltrande-Rio, H., Buxton, E.C., Edwards, J., Finch, R.A., Fridde, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jasing, C., Key, B.W., Jr., Kipp, P., Kohlhauf, B., Ma, Z.-Q., Markesich, D., Payne, R., Potter, D.G., Qian, N., Shaw, J., Schick, J., Shi, Z.-Z., Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N.,

TITLE Zhu, Q., Person, C. and Sands, A. T.
 wnt1 kinase deficiency lowers blood pressure in mice: a gene-trap
 screen to identify potential targets for therapeutic intervention
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
 COMMENT Contact: Zambrowicz BP
 OmniBank

Lexicon Genetics Incorporated
 4000 Research Forest Drive, The Woodlands, TX 77381, USA
 Email: materials@lexgen.com
 Gene trap sequence tag generated by 3' RACE from mouse ES cells as
 described in Zambrowicz et al (Nature, 1998 Apr 9;392(6676):608-11)
 Class: Gene trap.

FEATURES

source

Location/Qualifiers
 1..65
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="129Sv/Ev"
 /db_xref="taxon:10090"
 /clone="OST283929"
 /cell_type="embryonic stem cell"
 /clone_lib="Mus musculus 129Sv/Ev"

ORIGIN

Query Match 72.9%; Score 12.4; DB 9; Length 65;
 Best Local Similarity 57.1%; Pred. No. 9.3e+04;
 Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 3 UGAUUCUUCGAG 16
 :|||:|||||:
 Db 8 TGATTCTACTGCAG 21

RESULT 27

AL853876 67 bp mRNA linear EST 02-DEC-2003
 LOCUS AL853876 XGC-egg Xenopus tropicalis cDNA clone TB99005021 3', mRNA
 DEFINITION sequence.

ACCESSION AL853876 GI:38629511
 VERSION AL853876.2
 KEYWORDS EST.
 SOURCE Xenopus tropicalis (western clawed frog)
 ORGANISM Xenopus tropicalis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 Xenopodinae; Xenopus; Silurana.
 1 (bases 1 to 67)
 Crouching M.D.R., Ashurst J.L., Taylor R., Zorn, A.M. and Rogers, J.
 Sanger Xenopus tropicalis EST project 2001 (11_2003)
 JOURNAL Unpublished (2003)
 COMMENT On Sep 15, 2002 this sequence version replaced gi:22874096.
 Contact: Taylor R
 Sanger Institute
 Hinxton, Cambridgeshire, CB10 1SA, UK
 Email: trop@sanger.ac.uk
 Sanger Xenopus tropicalis EST project 2001
 TROPICALIS SEQUENCE ID: TB99005021.q1k17
 Sequencing primer: 77
 This sequence is from a Xenopus Gene Collection (XGC) library
 constructed by Aaron M. Zorn.
 cDNA was oligo dt primed from 5ug of poly A+ RNA from egg.
 EcoRI-NciI cut cDNA was then ligated into pCS107 with EcoRI at the
 5' end and NciI at the 3' end.
 Vector: pCS107; Site 1: EcoRI; Site 2: NciI
 Host: Escherichia coli XL1-blue.
 Location/Qualifiers
 1..67
 /organism="Xenopus tropicalis"
 /mol_type="mRNA"
 /db_xref="taxon:8364"
 /clone="TB99005021"
 /dev_stage="egg"
 /lab_host="Escherichia coli XL1-blue"
 /clone_lib="XGC-egg"

FEATURES

source

Location/Qualifiers
 1..67
 /organism="Xenopus tropicalis"
 /mol_type="mRNA"
 /db_xref="taxon:8364"
 /clone="TB99005021"
 /dev_stage="egg"
 /lab_host="Escherichia coli XL1-blue"
 /clone_lib="XGC-egg"

/note="Vector: pCS107; Site 1: EcoRI; Site 2: NciI; cDNA
 was oligo dt primed from 5ug of poly A+ RNA from egg.
 EcoRI-NciI cut cDNA was then ligated into pCS107 with
 EcoRI at the 5' end and NciI at the 3' end"

ORIGIN

Query Match 72.9%; Score 12.4; DB 1; Length 67;
 Best Local Similarity 57.1%; Pred. No. 9.3e+04;
 Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 2 CUGAUUCUUCGCA 15
 :|||:|||||:
 Db 41 CTGATTGCATTGCA 54

RESULT 28

BM514574/c 74 bp mRNA linear EST 15-FEB-2002
 LOCUS BM514574.1 Parastrongyloides trichosuri PA SL1 TOPO v1 Murphy
 DEFINITION Chiapelli McCarter Parastrongyloides trichosuri cDNA 5', mRNA
 sequence.

ACCESSION BM514574 GI:18685717
 VERSION BM514574.1
 KEYWORDS EST.
 SOURCE Parastrongyloides trichosuri
 ORGANISM Parastrongyloides trichosuri

Eukaryota; Metazoa; Chromadorea; Rhabditida;
 Panagrolaimidae; Strongyloidea; Parastrongyloides.
 1 (bases 1 to 74)
 McCarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J.,
 Wylie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B.,
 Bowers, Y., Gibbons, M., Ritter, E., Bennett, D., Franklin, C.,
 Tsagaris, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C.,
 Underwood, K., Stepien, M., Allen, M., Person, B., Swaller, T.,
 Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
 McCann, R., Waterston, R. and Wilson, R.
 The Washington Univ. Nematode EST Project, 1999
 Unpublished (1999)
 JOURNAL Contact: McCarter JP
 The Washington Univ. Nematode EST Project, 1999
 COMMENT The Washington Univ. Nematode EST Project, 1999
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 Nematodes provided by Dr. Warwick Grant of AgResearch, New Zealand
 (warwick.grant@agresearch.co.nz). The library was constructed by
 Brandi Chiapelli and Dr. James McCarter (bchiapell@watson.wustl.edu
 and jmcarter@watson.wustl.edu) at Washington University, St. Louis.
 DNA Sequencing by: Washington University Genome Sequencing Center
 St. Louis
 Seq primer: SL1 primer.
 Location/Qualifiers
 1..74
 /organism="Parastrongyloides trichosuri"
 /mol_type="mRNA"
 /db_xref="taxon:131310"
 /dev_stage="Parasitic adults"
 /lab_host="DH10B"
 /clone_lib="Parastrongyloides trichosuri PA SL1 TOPO v1
 Murphy Chiapelli McCarter"
 /note="Vector: pCRII-TOPO (Invitrogen); Site 1: EcoRI; The
 library was constructed by Claire Murphy, Brandi
 Chiapelli, and Dr. James McCarter at Washington
 University, St. Louis. Oligo(dt)-SL1 PCR based library.
 Parastrongyloides trichosuri parasitic adult cDNA PCR
 products of size >400 nucleotides containing SL1 on the 5'
 end and oligo(dt) on the 3' end were non-directionally
 cloned into pCRII-TOPO(Invitrogen) following the TOPO TA
 cloning protocol. Nematodes were provided by Dr. Warwick
 Grant of AgResearch, New Zealand
 (warwick.grant@agresearch.co.nz). Worms were harvested
 from Australian Brush-tailed possum (Trichosuri vulpecula)

and washed thoroughly to remove host contamination. Note that despite this effort, host contamination of the library is possible."

ORIGIN

Query Match 72.9%; Score 12.4; DB 4; Length 74;
Best Local Similarity 50.0%; Pred. No. 9.4e+04;
Matches 7; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
QY 2 CUGAUNUCAUUGCA 15
Db 25 CTGATTCATTCCTCA 12

RESULT 29

LOCUS AZ468373/c 74 bp DNA linear GSS 04-OCT-2000
DEFINITION 1M0281A22F Mouse 10kb plasmid UGCGIM library Mus musculus genomic
clone UGCGIM0281A22 F, genomic survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

1 (bases 1 to 74)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niederhausen, A. and Wright, D., Weiser, R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

TITLE

Unpublished (2000)

JOURNAL

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0281 row: A column: 22
Seq primer: CGTTGTAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 74.
Location/Qualifiers

FEATURES

source

1. 74
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGCGIM0281A22"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PMD42ny; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (gi|4732114|gb|AF128072.1), a copy-number
inducible derivative of plasmid RI. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to

adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Query Match 72.9%; Score 12.4; DB 8; Length 74;
Best Local Similarity 50.0%; Pred. No. 9.4e+04;
Matches 7; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
QY 1 CCUGAUNUCAUUGC 14
Db 23 CCGATTCATTCCTC 10

RESULT 30

LOCUS BZ593321 77 bp DNA linear GSS 07-JAN-2003
DEFINITION SALK_070016.16.25 x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_070016.16.25.x, genomic
survey sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

1 (bases 1 to 77)
Alonso, J.M., Leisner, T.J., Barajas, P., Chen, H., Cheuk, R.,
Gadriab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,
Shim, P., Zimmerman, J. and Ecker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)

TITLE

Unpublished (2001)

JOURNAL

COMMENT

Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA.
Class: TDNA tagged.
Location/Qualifiers

FEATURES

source

1. 77
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_070016.16.25.x"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match 72.9%; Score 12.4; DB 8; Length 77;
Best Local Similarity 50.0%; Pred. No. 9.5e+04;
Matches 7; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
QY 2 CUGAUNUCAUUGCA 15
Db 57 CTGATTCATTCCTCA 70

RESULT 31

LOCUS AW672652/c 79 bp mRNA linear EST 26-SEP-2001

DEFINITION	1x Explanted metanephric mesenchyme induced to differentiate into epithelial structures of the nephron ex vivo. Rattus norvegicus cDNA similar to similar to: gb U65091.1 MMUS5091 Mus musculus melanocyte-specific gene 1 (msg1) mRNA, mRNA sequence.			
ACCESSION	AW672652.1 GI:7541132			
VERSION	EST.			
KEYWORDS	Rattus norvegicus (Norway rat)			
SOURCE	Rattus norvegicus			
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
REFERENCE	1 (baes 5 to 79)			
AUTHORS	Pilsnov,S.Y., Ivanov,S.V., Yoshino,K., Dove,L.F., Pilsnova,T.M., Higginbotham,K.G., Kavaranova,I., Lerman,M. and Perantoni,A.O.			
TITLE	Mesenchymal-epithelial transition in the developing metanephric kidney: gene expression study by differential display			
JOURNAL	Genesis 27 (1), 22-31 (2000)			
MEDLINE	20321327			
PUBMED	10862152			
COMMENT	Contact: Pilsnov S.Y. Laboratory of Comparative Carcinogenesis National Cancer Institute FCBDC, Bldg.538, Room 205, Frederick, MD 21702, USA Tel: 301 846 1242 Fax: 301 846 4956 Email: pilsnov@mail.ncifcrf.gov PCR Primers FORWARD: ctgagcgcagctac BACKWARD: ttaagcttttttcta Insert Length: 79 Std Error: 0.00 Seq primer: SP6 High quality sequence stop: 79. Location/Qualifiers 1..79 /organism="Rattus norvegicus" /mol_type="mRNA" /db_xref="taxon:10116" /tissue_type="Metanephric mesenchyme" /cell_type="Mesenchymal/Epithelial" /dev_stage="13 dpc-16dpc" /lab_host="JMI09" /clone_idb="Explanted metanephric mesenchyme induced to differentiate into epithelial structures of the nephron ex vivo." /note="Organ: Kidney; Vector: pGEM-Teasy (Promega).; Restriction Enzymes 1; ApaI, AatII, SphI, NcoI, BstXI, NotI, SacII, and EcoRI SpeI, EcoRI, NotI, BstXI, PstI, SalI, NdeI, SacI, BstXI, and NotI cDNA fragment PCR-amplified in mRNA differential display analysis; cloned in pGEM-Teasy (Promega); its expression is developmentally regulated during mesenchymal-epithelial conversion in the metanephric kidney."			
ORIGIN				
Query Match	72.9%	Score 12.4;	DB 2;	Length 79;
Best Local Similarity	57.1%;	Pred. No. 9.5e+04;		
Matches	8;	Conservative 5;	Mismatches 1;	Indels 0;
Gaps	0;			
Db	35	GGATTTCACCTGCAG	22	
RESULT 32				
LOCUS	BU925856			
DEFINITION	88s83a10.y1 Gm-cl036 Glycine max cDNA SOYBEAN CLONE ID:			
ACCESSION	Gm-cl036-10771 5', mRNA sequence.			
VERSION	BU925856			
KEYWORDS	EST.			
SOURCE	Glycine max (soybean)			

ORGANISM	REFERENCE	TITLE	JOURNAL	COMMENT
Glycine max				
Eukaryotes: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.				
1 (bases 1 to 80)				
Shoenemaker, R., Keim, P., Vodkin, L., Expelding, J., Coryell, V., Khanna, A., Bolla, B., Marras, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, J., Peterson, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurr, R., Ritzler, E., Kohn, S., Shih, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.				
Public Soybean EST Project				
Unpublished (1999)				
Contact: Shoenemaker R/Public Soybean EST Project				
Public Soybean EST Project				
Washington University School of Medicine				
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA				
Tel: 314 286 1800				
Fax: 314 286 1810				
Email: est@watson.wustl.edu				
When it has been determined, an EST from the other end of this clone is listed in the 'Other ESTs on clone' field. This clone is available through: Biogenetic Services, 801 3nd Ave, Brookings, SD 57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)				
Putative full length read vector to vector length is 81				
Seq primer: -40RP from Gibco.				
Location/Qualifiers				
1..80				

```

/clone="SOYBEAN CLONE ID: Gm-cl036-107721"
/tissue_type="somatic embryos cultured on MSD 20"
/lab_host="DH10B"
/clone_id="Gm-cl036"
/notes="Vector: pSPORT1; Site 1: NotI; Site 2: SalI; This
cDNA library was constructed from mRNA isolated from
somatic embryos (age ranging from 2 months to 9 months)
cultured on MSD 20. The library was prepared using the
Life Technologies psuperScript cDNA library construction
kit. Complementary DNA was synthesized from mRNA using a
poly (dT) sequence with a NotI restriction site. SalI
linkers adapters were ligated to the blunt-ended cDNA
fragments followed by NotI digestion. The cDNA fragments
were directionally cloned into the NotI-SalI restriction
site of the pSPORT1 vector. The ligated cDNA fragments
were transformed into E.coli Electromax DH10B host cells.
This library was constructed in the laboratory of Dr. Lita
Vodkin by Anu Khanna at the University of Illinois at
Urbana-Champaign. e-mail: l-vodkin@uiuc.edu"

```

REFERENCE
AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 81)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamli, C., Irlam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weis, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL
COMMENT

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genome.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0070 row: M column: 06
Seq primer: CACACGAAACAGCATGACC
Class: plasmid ends
High quality sequence stop: 81.

FEATURES
source

Location/Qualifiers
1..81
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U08C1M0070M06"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
/note="Vector: PMD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid RI. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 72.9%; Score 12.4; DB 8; Length 81;
Best Local Similarity 50.0%; Pred. No. 9.6e+04;
Matches 7; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCUGAUTCATGCG 14
||:||||:||||
DB 73 CTTGATTCATGCG 60

RESULT 34
LOCUS BZ587139 82 bp DNA linear GSS 17-DEC-2002
DEFINITION 3590_1_10_1_C02_2EL_x_1_3590 - Rescuedu Grid M Zea mays genomic,
ACCESSION BZ587139
VERSION BZ587139.1 GI:27222200
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays

REFERENCE

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD clade; Panicoideae; Andropogoneae; Zea. 1 (bases 1 to 82)
Walbot, V.
Maize genomic sequences found using engineered Rescuedu transposon
Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu

JOURNAL
COMMENT

Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 3590_1_10_1 column: 11
Class: transposon-tagged.

FEATURES
source

Location/Qualifiers
1..82
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_11b="3590 - Rescuedu Grid M"
/note="Organ: leaf; Vector: Rescuedu (engineered from pBluescript backbone); Site 1: BamHI; Site 2: BglII; Rescuedu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on Rescuedu, go to the web site 'www.zmdb.iastate.edu' and follow the links for 'Rescuedu'. Grid M was grown at University of Arizona in 2001. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmid. DH10B cells were transformed and then screened on LB plates with ampicillin."

ORIGIN

Query Match 72.9%; Score 12.4; DB 8; Length 82;
Best Local Similarity 50.0%; Pred. No. 9.6e+04;
Matches 7; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCUGAUTCATGCG 14
||:||||:||||
DB 57 CCGGTTTCATGCG 44

RESULT 35
LOCUS CN855612 83 bp mRNA linear EST 03-JUN-2004
DEFINITION 000721AA002844HT (AAA) Royal Gala 59 DAFB fruit, seeds removed
ACCESSION CN855612
VERSION CN855612.1 GI:48110989
KEYWORDS EST.
SOURCE Malus x domestica (cultivated apple)
ORGANISM Malus x domestica

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosid 1; Rosales; Rosaceae; Maloideae; Malus. 1 (bases 1 to 83)
Benning, L., Bowen, J., Crowhurst, R., Gleeve, A., Janssen, B., McArtney, S., Newcomb, R., Ross, G., Snowden, K., Walton, E. and Yauk, Y.
HortResearch Apple EST Project
Unpublished (2004)
Contact: Gleeve, A.
Sequencing Facility
The Horticulture and Food Research Institute of New Zealand Ltd
120 Mt Albert Rd, Mt Albert, Auckland, New Zealand

Tel: 00 64 09 815 4200
Fax: 00 64 09 815 4201
Email: es@hortresearch.co.nz.
Location/Qualifiers

FEATURES

source

1. 83
/organism="Mus x domestica"
/mol_type="mRNA"
/db_xref="taxon:3750"
/clone="AAAA02844"
/tissue_type="fruit"
/dev_stage="59 days after full bloom, seeds removed"
/clone_11b="(AAAA) Royal Gala 59 DAFB fruit, seeds removed"
/note="Vector: PBK-CMV; library sequenced by Genesis Research & Development"

ORIGIN

Query Match 72.9%; Score 12.4; DB 7; Length 83;
Best Local Similarity 50.0%; Pred. No. 9.6e+04;
Matches 7; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

OY 3 UGAUUCACUUGCAG 16
: ||::||::||::||
14 TCCTTCATTGCAG 1

RESULT 36 BH791384 83 bp DNA linear GSS 02-APR-2002
LOCUS SALK_059855.54.50.x Arabidopsis thaliana TDNA insertion lines
DEFINITION Survey sequence.
Arabidopsis thaliana genomic clone SALK_059855.54.50.x, genomic survey sequence.

ACCESSION BH791384.1 GI:19885192
VERSION BH791384

KEYWORDS Arabidopsis thaliana (thale cress)

SOURCE

Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 83)

REFERENCE Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadinh,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shim,P., Zimmerman,J. and Ecker,J.R.

TITLE A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome

JOURNAL

COMMENT Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: eckere@salic.edu

COMMENT

This is single pass sequence recovered from the left border of
TDNA. This sequence lies within an annotated intron of At5g44580.
Class: TDNA tagged.
Location/Qualifiers

FEATURES

source

1. 83
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_059855.54.50.x"
/clone_11b="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/cdna_protocols.html"

ORIGIN

Query Match 72.9%; Score 12.4; DB 8; Length 83;
Best Local Similarity 57.1%; Pred. No. 9.6e+04;
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 2 CUGAUUCACUUGCA 15
: ||::||::||::||
42 CCGATTTCATTGCA 29

RESULT 37 AZ820505 91 bp DNA linear GSS 20-FEB-2001
LOCUS 2M0092P06R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC2M0092P06 R, genomic survey sequence.
AZ820505
AZ820505.1 GI:12990329

ACCESSION GSS.
VERSION Mus musculus (house mouse)
KEYWORDS Mus musculus
SOURCE Mus musculus

ORGANISM

REFERENCE

AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamill,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts

JOURNAL

COMMENT

Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLG, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
Plate: 0092 row: P column: 06
Seq primer: CACACAGGAACACGCTATGACC
Class: plasmid ends
High quality sequence stop: 91.
Location/Qualifiers

FEATURES

source

1. 91
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0092P06"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv, Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(<http://www.jax.org/resources/documents/dnares/>). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD19 (gii473211|gb|AF12972.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Query Match 72.9%; Score 12.4; DB 8; Length 91;
 Best Local Similarity 57.1%; Pred. No. 9.7e+04;
 Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 4 GAUUCAUUGCAGG 17
 |||:|||||
 23 GATTTCATTACAGG 36

RESULT 38
 C00319/c 96 bp mRNA linear EST 31-DEC-2002
 LOCUS HUMS0006024 Human adult (K.Okubo) Homo sapiens cDNA, mRNA
 DEFINITION sequence.
 ACCESSION C00319
 VERSION C00319.1 GI:1432549
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 96)
 Okubo, K. human gene expression database
 Unpublished (1995)
 CONTACT: Okubo, K.
 Institute for Molecular and Cellular Biol
 Osaka University
 1-3, Yamada-oka, Suita, Osaka Pref. 565, Japan
 Tel: 06-877-5111 (ex.3315)
 Email: koueak@imcb.osaka-u.ac.jp
 We are not submitting the same cDNA sequence redundantly to DBJ
 since 1993. For the abundance information of clones with this
 sequence in this library and as well as in other 3'-directed
 libraries, see: <http://www.imcb.osaka-u.ac.jp/bodymap>. The
 sequences of the clones represented by this GS sequences is also
 found there.

FEATURES
 source Location/Qualifiers
 1..96
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="adult"
 /clone_lib="Human adult (K.Okubo)"
 /note="One or more human adult tissue"

ORIGIN
 Query Match 72.9%; Score 12.4; DB 6; Length 96;
 Best Local Similarity 50.0%; Pred. No. 9.8e+04;
 Matches 7; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCUGAUTCNUCC 14
 |||:|||||
 47 CCTGATTCATTC 34

RESULT 39
 CV296295/c 96 bp mRNA linear EST 23-SEP-2004
 LOCUS EST84672 petunia floral development cDNA library Petunia x hybrida
 DEFINITION cDNA clone Petunia-DeVA-12-B07 5' end, mRNA sequence.
 ACCESSION CV296295
 VERSION CV296295.1 GI:52587436
 KEYWORDS EST.
 SOURCE Petunia x hybrida
 ORGANISM Petunia x hybrida
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; lamiales; Solanales; Solanaceae; Petunia.
 1 (bases 1 to 96)
 Shibuya, K., Underwood, B., Loucas, H., Farmerie, W., Jones, M. and
 Clark, D.
 Petunia x hybrida EST collection

JOURNAL
 COMMENT Unpublished (2004)
 Contact: David Clark
 UF Floriculture Biotechnology Lab
 University of Florida
 Environmental Horticulture Department, 1545 Piffeld Hall, Box
 110670, Gainesville, FL 32611-0670, USA
 Tel: 352-392-1831 x370
 Fax: 352-392-3870
 Email: dclark@mail.ifas.ufl.edu
 Contact Dr. Clark (dclark@mail.ifas.ufl.edu) for clone information
 Seq primer: T3 primer.

FEATURES
 source Location/Qualifiers
 1..96
 /organism="Petunia x hybrida"
 /mol_type="mRNA"
 /cultivar="Mitchell Diploid (aka. Mitchell, aka W115 in
 Europe)"
 /db_xref="taxon:4102"
 /clone="petunia-DeVA-12-B07"
 /tissue_type="all floral organs"
 /lab_host="lambda ZAPII unidirectional"
 /clone_lib="petunia floral development cDNA library"
 /note="Vector: pBluescript SK-; Site 1: EcoRI, Site 2:
 XhoI; supplier: Petunia x hybrida cv. Mitchell Diploid
 plants were grown from seeds to a fully flowering stage
 under standard greenhouse conditions. Ten entire flowers
 of six developmental stages were collected on the same day
 from plants grown in standard greenhouses. The flower
 stages were as follows in chronological order from
 youngest to oldest: stage 1 - no color in corolla; corolla
 0.5 inches long stage 2 - first sign of color in corolla;
 corolla .75-1 inches long stage 3 - fully elongated
 corolla (not open); corolla 1.5 inches long stage 4 -
 fully open corolla; anthers not yet dehiscent stage 5 -
 fully open corolla; freshly anthesed, bright yellow
 pollen; wet stigma stage 6 - pre-senescent; yellowing of
 corolla tube; dry brown pollen (if present); stigma dry.
 Total RNA was extracted from each sample, and 100
 micrograms of each sample was combined for subsequent poly
 A+ mRNA selection and cDNA synthesis."

ORIGIN
 Query Match 72.9%; Score 12.4; DB 7; Length 96;
 Best Local Similarity 50.0%; Pred. No. 9.8e+04;
 Matches 7; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 2 CUGAUTCNUCCA 15
 |||:|||||
 84 CTGATTCATTGTA 71

RESULT 40
 BI090229/c 98 bp mRNA linear EST 20-JUN-2001
 LOCUS 602857182F1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:498476 5',
 DEFINITION mRNA sequence.
 ACCESSION BI090229
 VERSION BI090229.1 GI:14508559
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 98)
 NIH-MGC <http://mgc.ncl.nih.gov/>,
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cga@bcr-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: Incyte Genomics, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:

http://image.lnl.gov

Plate: L1AM1027 row: c column: 21
High quality sequence stop: 98.

FEATURES

Source

Location/Qualifiers

1..98

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4998476"

/cell_line="MGC36"

/lab_host="DH10B"

/clone_lib="NIH_MGC_10"

/note="Organ: cervix; Vector: PCMV-SPORT6; Site 1: NotI;

Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.

Average insert size 1.5 kb. Library prepared by Life

Technologies."

ORIGIN

Query Match

72.9%; Score 12.4; DB 4; Length 98;

Best Local Similarity 50.0%; Pred. No. 9.9e+04;

Matches 7; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCTGAUUDCAUUGC 14

Db 31 CCTGATTCATATCC 18

Search completed: May 13, 2005, 17:50:53
Job time : 845.127 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 13, 2005, 16:49:04 ; Search time 1090.95 Seconds
(without alignments)
1687.800 Million cell updates/sec

Title: US-09-927-046-2332

Perfect score: 38
Sequence: 1 ccgcaucgaugagcgccguuagcgcaaaaacag 38

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 2238514

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :
1: gb_da:*
2: gb_hlg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_scs:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	100.0	38	6	AX580494 Sequence
2	36	94.7	37	6	AX583594 Sequence
3	31.8	83.7	38	6	AX218695 Sequence
4	31.4	82.6	38	6	AX218894 Sequence
5	31.4	82.6	38	6	AX273385 Sequence
6	31.4	82.6	38	6	AX580466 Sequence
7	31.2	82.1	38	6	AR331496 Sequence
8	31.2	82.1	38	6	AR331983 Sequence
9	30.8	81.1	38	6	AR330070 Sequence
10	30.8	81.1	38	6	AR331271 Sequence
11	30.6	80.5	38	6	AR332172 Sequence
12	30.4	80.0	38	6	AR332011 Sequence
13	30.4	80.0	38	6	AR333161 Sequence
14	30.4	80.0	38	6	AX218945 Sequence
15	30.4	80.0	38	6	AX219642 Sequence
16	30.4	80.0	38	6	AX222387 Sequence
17	30.2	79.5	38	6	AR330741 Sequence
18	30.2	79.5	38	6	AX219074 Sequence
19	30	78.9	38	6	AR330124 Sequence

20	30	78.9	38	6	AR330364 Sequence
21	30	78.9	38	6	AR332137 Sequence
22	30	78.9	38	6	AX227896 Sequence
23	30	78.9	38	6	AX580822 Sequence
24	29.8	78.4	38	6	AR330838 Sequence
25	29.8	78.4	38	6	AR330943 Sequence
26	29.8	78.4	38	6	AR331128 Sequence
27	29.8	78.4	38	6	AX218680 Sequence
28	29.8	78.4	38	6	AX218848 Sequence
29	29.8	78.4	38	6	AX219667 Sequence
30	29.8	78.4	38	6	AX222419 Sequence
31	29.6	77.9	38	6	AR331511 Sequence
32	29.6	77.9	38	6	AX218714 Sequence
33	29.6	77.9	38	6	AX218873 Sequence
34	29.6	77.9	38	6	AX219601 Sequence
35	29.6	77.9	38	6	AX222613 Sequence
36	29.6	77.9	38	6	AX227899 Sequence
37	29.6	77.9	38	6	AX580764 Sequence
38	29.6	77.9	38	6	AX580873 Sequence
39	29.4	77.4	38	6	AR330254 Sequence
40	29.4	77.4	38	6	AR330461 Sequence
41	29.4	77.4	38	6	AR331020 Sequence
42	29.4	77.4	38	6	AR331551 Sequence
43	29.4	77.4	38	6	AR332105 Sequence
44	29.4	77.4	38	6	AR332157 Sequence
45	29.4	77.4	38	6	AR333898 Sequence
46	29.4	77.4	38	6	AX219574 Sequence
47	29.4	77.4	38	6	AX423799 Sequence
48	29.4	77.4	38	6	AX581103 Sequence
49	29.2	76.8	38	6	AR046961 Sequence
50	29.2	76.8	38	6	154013 Sequence 17
51	29.2	76.8	38	6	AR330896 Sequence
52	29.2	76.8	38	6	AR331305 Sequence
53	29.2	76.8	38	6	AR332219 Sequence
54	29.2	76.8	38	6	AX218704 Sequence
55	29.2	76.8	38	6	AX218736 Sequence
56	29.2	76.8	38	6	AX218962 Sequence
57	29.2	76.8	38	6	AX219605 Sequence
58	29.2	76.8	38	6	AX222374 Sequence
59	29.2	76.8	38	6	AX222478 Sequence
60	29.2	76.8	38	6	AX227940 Sequence
61	29.2	76.8	38	6	AX228365 Sequence
62	29	76.3	38	6	AR331384 Sequence
63	29	76.3	38	6	AR333453 Sequence
64	29	76.3	38	6	AR335862 Sequence
65	29	76.3	38	6	AX218598 Sequence
66	29	76.3	38	6	AX218781 Sequence
67	29	76.3	38	6	AX218967 Sequence
68	29	76.3	38	6	AX423865 Sequence
69	29	76.3	38	6	AX424179 Sequence
70	29	76.3	38	6	AX580589 Sequence
71	28.8	75.8	38	6	AR330131 Sequence
72	28.8	75.8	38	6	AR330645 Sequence
73	28.8	75.8	38	6	AR330926 Sequence
74	28.8	75.8	38	6	AR332998 Sequence
75	28.8	75.8	38	6	AR333246 Sequence
76	28.8	75.8	38	6	AR333642 Sequence
77	28.8	75.8	38	6	AR334821 Sequence
78	28.8	75.8	38	6	AR335093 Sequence
79	28.8	75.8	38	6	AR336492 Sequence
80	28.8	75.8	38	6	AX218596 Sequence
81	28.8	75.8	38	6	AX218612 Sequence
82	28.8	75.8	38	6	AX218613 Sequence
83	28.8	75.8	38	6	AX218829 Sequence
84	28.8	75.8	38	6	AX218972 Sequence
85	28.8	75.8	38	6	AX222333 Sequence
86	28.8	75.8	38	6	AX227877 Sequence
87	28.8	75.8	38	6	AX228151 Sequence
88	28.8	75.8	38	6	AX228186 Sequence
89	28.8	75.8	38	6	AX423978 Sequence
90	28.8	75.8	38	6	AX580357 Sequence
91	28.8	75.8	38	6	AX580573 Sequence
92	28.6	75.3	38	6	AR330224 Sequence

93 28.6 75.3 38 6 AR330756 Sequence
94 28.6 75.3 38 6 AR330934 Sequence
95 28.6 75.3 38 6 AR331361 Sequence
96 28.6 75.3 38 6 AR331857 Sequence
97 28.6 75.3 38 6 AR331852 Sequence
98 28.6 75.3 38 6 AX222647 Sequence
99 28.6 75.3 38 6 AX222769 Sequence
100 28.6 75.3 38 6 AX222850 Sequence

ALIGNMENTS

RESULT 1
AX580494 38 bp RNA linear PAT 10-JAN-2003
LOCUS Sequence 2332 from Patent WO0211674.
ACCESSION AX580494
VERSION AX580494.1 GI:27649696
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 Thompson,J., Mcswigen,J., McKenzie,T., Ayers,D., Szymkowski,D.E. and Grube,A.
AUTHORS Method and reagent for the inhibition of calcium activated chloride channel-1 (Clca-1)
TITLE Patent: WO 0211674-A 2332 14-FEB-2002;
JOURNAL RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ; Thompson, James (US)
FEATURES
source 1..38
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Enzymatic Nucleic Acid"
ORIGIN
Query Match 100.0%; Score 38; DB 6; Length 38;
Best Local Similarity 81.6%; Pred. No. 1.7e-05;
Matches 31; Conservative 7; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCUGCAUCUGAUGAGCGCGUUGAGCCGAAAAUACAG 38
Db 1 CCTGCAATCTGATGAGCGCGTTAGCGCGAAAAATCAG 38
RESULT 2
AX583594 37 bp RNA linear PAT 10-JAN-2003
LOCUS Sequence 5432 from Patent WO0211674.
ACCESSION AX583594
VERSION AX583594.1 GI:27655404
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 Thompson,J., Mcswigen,J., McKenzie,T., Ayers,D., Szymkowski,D.E. and Grube,A.
AUTHORS Method and reagent for the inhibition of calcium activated chloride channel-1 (Clca-1)
TITLE Patent: WO 0211674-A 5432 14-FEB-2002;
JOURNAL RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ; Thompson, James (US)
FEATURES
source 1..37
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Enzymatic Nucleic Acid"
misc_feature 1..8

misc_feature /note="2'-O-Methyl"
misc_feature 1..4
/note="Phosphorothioate 3'-internucleotide linkage"
misc_feature 9
/note="2'-deoxy-2'-C-Allyl"
misc_feature 12
/note="2'-O-Methyl"
misc_feature 14..26
/note="2'-O-Methyl"
misc_feature 28..29
/note="2'-O-Methyl"
misc_feature 31..36
/note="2'-O-Methyl"
misc_feature 37
/note="n strands for inverted deoxyabasic derivative"
ORIGIN
Query Match 94.7%; Score 36; DB 6; Length 37;
Best Local Similarity 80.6%; Pred. No. 0.00013;
Matches 29; Conservative 7; Mismatches 0; Indels 0; Gaps 0;
Qy 2 CUGCAUCUGAUGAGCGCGUUGAGCCGAAAAUACAG 37
Db 1 CTGCAATCTGATGAGCGCGTTAGCGCGAAAAATCAG 36
RESULT 3
AX218695 38 bp RNA linear PAT 07-SEP-2001
LOCUS Sequence 4137 from Patent WO0159103.
ACCESSION AX218695
VERSION AX218695.1 GI:15546419
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 Blatt,L., Mcswigen,J. and Chowrira,B.M.
AUTHORS Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
TITLE Patent: WO 0159103-A 4137 16-AUG-2001;
JOURNAL RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ; Mcswigen, James (US) ; Chowrira, Bharat M. (US)
FEATURES
source 1..38
/organism="synthetic construct"
/mol_type="unassigned RNA"
/db_xref="taxon:32630"
/note="Nucleic Acid"
ORIGIN
Query Match 83.7%; Score 31.8; DB 6; Length 38;
Best Local Similarity 74.3%; Pred. No. 0.0087;
Matches 26; Conservative 7; Mismatches 2; Indels 0; Gaps 0;
Qy 2 CUGCAUCUGAUGAGCGCGUUGAGCCGAAAAUACAG 36
Db 2 CTTTAATCTGATGAGCGCGTTAGCGCGAAAAATCA 36
RESULT 4
AX218894 38 bp RNA linear PAT 07-SEP-2001
LOCUS Sequence 4336 from Patent WO0159103.
ACCESSION AX218894
VERSION AX218894.1 GI:15546618
KEYWORDS
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 Blatt,L., Mcswigen,J. and Chowrira,B.M.
AUTHORS Method and reagent for the modulation and diagnosis of cd20 and

JOURNAL	nogo gene expression Patent: WO 0159103-A 436 16-AUG-2001;
RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ; McSwiggen, James (US) ; Chowrira, Bharat M. (US)	
FEATURES	
source	1..38 /organism="synthetic construct" /mol_type="unassigned RNA" /db_xref="taxon:32630" /note="Nucleic Acid"
ORIGIN	
Query Match	82.6%; Score 31.4; DB 6; Length 38;
Best Local Similarity	81.8%; Pred. No. 0.013; Indels 0; Gaps 0;
Matches	27; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
Db	5 CAUUCGAGUAGGCCCGUUAGCCCGAANAUAACG 37 :: :: :: :: :: 5 CAATCTGATGAGCCGTTAGGCCGAAAAGCAG 37
RESULT 5	
LOCUS	AX273385 38 bp RVA linear PAT 29-OCT-2001
DEFINITION	Sequence 954 from Patent WO0162911.
ACCESSION	AX273385
VERSION	AX273385.1 GI:16546122
KEYWORDS	.
SOURCE	synthetic construct
ORGANISM	synthetic construct
REFERENCE	other sequences; artificial sequences.
AUTHORS	1 Jarvik,T., von Carlowitz,I., Mcswiggen,J.A., Hamblin,P.A. and Ellis,J.H. Method and reagent for the inhibition of grid Patent: WO 0162911-A 954 30-AUG-2001; RIBOZYME PHARMACEUTICALS, INC. (US) ; GLAXO GROUP LIMITED (GB) Location/Qualifiers 1..38 /organism="synthetic construct" /mol_type="unassigned RNA" /db_xref="taxon:32630" /note="Enzymatic Nucleic Acid"
FEATURES	
source	1..38 /organism="synthetic construct" /mol_type="unassigned RNA" /db_xref="taxon:32630" /note="Enzymatic Nucleic Acid"
ORIGIN	
Query Match	82.6%; Score 31.4; DB 6; Length 38;
Best Local Similarity	78.8%; Pred. No. 0.013; Indels 0; Gaps 0;
Matches	26; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
Db	4 GCAAUUCGAGUAGGCCCGUUAGCCCGAANAUAUCA 36 :: :: :: :: :: 4 GCAGTCTGATGAGCCCGTTAGGCCGAANAATCA 36
RESULT 6	
LOCUS	AX580466 38 bp RNA linear PAT 10-JAN-2003
DEFINITION	Sequence 2304 from Patent WO0211674.
ACCESSION	AX580466
VERSION	AX580466.1 GI:27649668
KEYWORDS	.
SOURCE	synthetic construct
ORGANISM	synthetic construct
REFERENCE	other sequences; artificial sequences.
AUTHORS	1 Thompson,J., Mcswiggen,J., McKenzie,T., Ayers,D., Szymkowski,D.E. and Grupe,A. Method and reagent for the inhibition of calcium activated chloride channel-1 (Clca-1) Patent: WO 0211674-A 2304 14-FEB-2002; RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ; Thompson, James (US) Location/Qualifiers
TITLE	
JOURNAL	
FEATURES	

Source	1..38	/organism="synthetic construct"	/mol_type="unassigned RNA"	/db_xref="taxon:32630"	/note="Enzymatic Nucleic Acid"
ORIGIN					
Query Match	82.6%; Score 31.4; DB 6; Length 38;				
Best Local Similarity	75.0%; Pred. No. 0.013; Matches 25; Conservative 7; Mismatches 1; Indels 0; Gaps 0;				
Db	3 UGCAUUCUGAUGAGCCGCUUAGCCGAAAAAUC 35				
	3 TGAATCTGATGAGGCCGTTAGCCGAAATC 35				
RESULT 7					
AR331496	38 bp RNA	linear	PAT 17-AUG-2003		
LOCUS					
DEFINITION	Sequence 8898 from patent US 6566127.				
ACCESSION	AR331496				
VERSION	AR331496.1 GI:33717304				
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 38)				
AUTHORS	Pavco, P., McSwiggen, J. A., Stinchcomb, D. T. and Escobedo, J.				
TITLE	Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor				
JOURNAL	Patent: US 6566127-A 8898 20-MAY-2003;				
FEATURES	Location/Qualifiers				
source	1..38				
	/organism="unknown"				
	/mol_type="unassigned RNA"				
ORIGIN					
Query Match	82.1%; Score 31.2; DB 6; Length 38;				
Best Local Similarity	75.0%; Pred. No. 0.016; Matches 27; Conservative 6; Mismatches 3; Indels 0; Gaps 0;				
Db	1 CCUGCAUUCUGAUGAGCCCGUUNAGCCGAAAAAACA 36				
	1 CCTTCATCTGATGAGGCCGTTAGCCGAAAGACA 36				
RESULT 8					
AR331983	38 bp RNA	linear	PAT 17-AUG-2003		
LOCUS					
DEFINITION	Sequence 9385 from patent US 6566127.				
ACCESSION	AR331983				
VERSION	AR331983.1 GI:33717791				
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 38)				
AUTHORS	Pavco, P., McSwiggen, J. A., Stinchcomb, D. T. and Escobedo, J.				
TITLE	Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor				
JOURNAL	Patent: US 6566127-A 9385 20-MAY-2003;				
FEATURES	Location/Qualifiers				
source	1..38				
	/organism="unknown"				
	/mol_type="unassigned RNA"				
ORIGIN					
Query Match	82.1%; Score 31.2; DB 6; Length 38;				
Best Local Similarity	77.8%; Pred. No. 0.016; Matches 28; Conservative 5; Mismatches 3; Indels 0; Gaps 0;				
Db	1 CCUGCAUUCUGAUGAGCCCGUUNAGCCGAAAAAACA 36				
	1 CCTTCATCTGATGAGGCCGTTAGCCGAAAGACA 36				

Db 1 CCCGCAACTGATGAGCGCCGTTAGCGCGAAAGTCA 36

RESULT 9
AR330070 LOCUS AR330070 38 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 7472 from patent US 6566127.
ACCESSION AR330070
VERSION AR330070.1 GI:33715878
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 38)
TITLE Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
JOURNAL Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
FEATURES Patent: US 6566127-A 7472 20-MAY-2003;
Location/Qualifiers
1..38
/organism="unknown"
/mol_type="unassigned RNA"

ORIGIN
Query Match 81.1%; Score 30.8; DB 6; Length 38;
Best Local Similarity 76.5%; Pred. No. 0.024;
Matches 26; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CUGCAUCGAGGCGGCGUAGCGCGAAAUVC 35
Db 2 CCGCAGTCGATGAGCGCCGTTAGCGCGAAATC 35

RESULT 10
AR331271 LOCUS AR331271 38 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 8673 from patent US 6566127.
ACCESSION AR331271
VERSION AR331271.1 GI:33717079
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 38)
TITLE Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
JOURNAL Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
FEATURES Patent: US 6566127-A 8673 20-MAY-2003;
Location/Qualifiers
1..38
/organism="unknown"
/mol_type="unassigned RNA"

ORIGIN
Query Match 81.1%; Score 30.8; DB 6; Length 38;
Best Local Similarity 76.5%; Pred. No. 0.024;
Matches 26; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCUGCAUCGAGGCGGCGUAGCGCGAAAUVC 34
Db 1 CCTGCAAGCTGATGAGCGCCGTTAGCGCGAAAT 34

RESULT 11
AR332172 LOCUS AR332172 38 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 9574 from patent US 6566127.
ACCESSION AR332172
VERSION AR332172.1 GI:33717980
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.

REFERENCE 1 (bases 1 to 38)
AUTHORS Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
TITLE Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
JOURNAL Patent: US 6566127-A 9574 20-MAY-2003;
FEATURES Location/Qualifiers
1..38
/organism="unknown"
/mol_type="unassigned RNA"

ORIGIN
Query Match 80.5%; Score 30.6; DB 6; Length 38;
Best Local Similarity 70.3%; Pred. No. 0.029;
Matches 26; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

Qy 2 CUGCAUCGAGGCGGCGUAGCGCGAAAUVCAG 38
Db 2 CTCGATTCGATGAGCGCCGTTAGCGCGAAATGCGG 38

RESULT 12
AR332011 LOCUS AR332011 38 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 9413 from patent US 6566127.
ACCESSION AR332011
VERSION AR332011.1 GI:33717819
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 38)
TITLE Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
JOURNAL Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
FEATURES Patent: US 6566127-A 9413 20-MAY-2003;
Location/Qualifiers
1..38
/organism="unknown"
/mol_type="unassigned RNA"

ORIGIN
Query Match 80.0%; Score 30.4; DB 6; Length 38;
Best Local Similarity 81.2%; Pred. No. 0.036;
Matches 26; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCUGCAUCGAGGCGGCGUAGCGCGAAAUVC 32
Db 1 CCTGCAAGCTGATGAGCGCCGTTAGCGCGAAAU 32

RESULT 13
AR333161 LOCUS AR333161 38 bp RNA linear PAT 17-AUG-2003
DEFINITION Sequence 10563 from patent US 6566127.
ACCESSION AR333161
VERSION AR333161.1 GI:33718969
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
AUTHORS 1 (bases 1 to 38)
TITLE Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
JOURNAL Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor
FEATURES Patent: US 6566127-A 10563 20-MAY-2003;
Location/Qualifiers
1..38
/organism="unknown"
/mol_type="unassigned RNA"

ORIGIN
Query Match 80.0%; Score 30.4; DB 6; Length 38;
Best Local Similarity 81.2%; Pred. No. 0.036;

Qy	Db	Matches	26; Conservative	5; Mismatches	1; Indels	0; Gaps	0;
RESULT 14							
AX218945							
LOCUS	AX218945	38 bp			linear	PAT 07-SEP-2001	
DEFINITION	Sequence 4387 from Patent WO0159103.						
ACCESSION	AX218945						
VERSION	AX218945.1	GI:15546669					
KEYWORDS							
SOURCE							
ORGANISM							
REFERENCE							
AUTHORS	1						
TITLE	Blatt, L., McSwiggen, J. and Chowrira, B.M.						
JOURNAL	Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression						
Patent:	WO 0159103-A 4387 16-AUG-2001;						
RIBOZYME	PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;						
McSwiggen, James (US) ; Chowrira, Bharat M. (US)							
Location/Qualifiers							
1..38							
/organism="synthetic construct"							
/mol_type="unassigned RNA"							
/db_xref="taxon:32630"							
/note="Nucleic Acid"							
modified_base	31						
/mod_base=1							
ORIGIN							
Query Match		80.0%;	Score 30.4;	DB 6;	Length 38;		
Best Local Similarity		81.2%;	Pred. No. 0.036;				
Matches	26; Conservative	5; Mismatches	1; Indels	0; Gaps	0;		
Qy	5	CAUTCUGAUGAGCCGCUUAGCCGCAAAAAUCA	36				
Db	5	CAACCTGATGAGCGCGTTAGCCGAAAAATCA	36				
RESULT 15							
AX219642							
LOCUS	AX219642	38 bp			linear	PAT 07-SEP-2001	
DEFINITION	Sequence 5084 from Patent WO0159103.						
ACCESSION	AX219642						
VERSION	AX219642.1	GI:15547366					
KEYWORDS							
SOURCE							
ORGANISM							
REFERENCE							
AUTHORS	1						
TITLE	Blatt, L., McSwiggen, J. and Chowrira, B.M.						
JOURNAL	Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression						
Patent:	WO 0159103-A 5084 16-AUG-2001;						
RIBOZYME	PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;						
McSwiggen, James (US) ; Chowrira, Bharat M. (US)							
Location/Qualifiers							
1..38							
/organism="synthetic construct"							
/mol_type="unassigned RNA"							
/db_xref="taxon:32630"							
/note="Nucleic Acid"							
modified_base	31						
/mod_base=1							
ORIGIN							
Query Match		80.0%;	Score 30.4;	DB 6;	Length 38;		
Best Local Similarity		75.8%;	Pred. No. 0.036;				
Matches	25; Conservative	6; Mismatches	2; Indels	0; Gaps	0;		
Qy	2	CUGCAUUCUGAUGAGCCGCUUAGCCGCAAAAAU	34				

[illegible]

VERSION	AX219074.1	GI:15546798
KEYWORDS	synthetic construct	
SOURCE	other sequences; artificial sequences.	
ORGANISM	Blatt,L., Mcswiggen,J. and Chowrira,B.M. Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression Patent: WO 0159103-A 4516 16-AUG-2001; RHOZYME PHARMACEUTICALS, INC. (US); Blatt, Lawrence (US) ; McSwiggen, James (US) ; Chowrira, Bharat M. (US)	
REFERENCE AUTHORS TITLE	Location/Qualifiers	
JOURNAL	1..38	
FEATURES source	/organism="synthetic construct" /mol_type="unassigned RNA" /db_xref="taxon:32630" /note="Nucleic Acid"	
ORIGIN		
Query Match	79.5%; Score 30.2;	DB 6;
Best Local Similarity	74.3%; Pred. No. 0.044;	Length 38;
Matches	26; Conservative	6; Mismatches 3; Indels 0; Gaps 0;
Dy	<pre>2 CUCGAUUCUGAUGAGCCGCGUAGGCCGAAAUCA 36 : : :: :: :: :: : 2 CTGC AACCTGATGAGC CGTTAGCGCGAAAATAA 36</pre>	
RESULT 19		
AR330124	38 bp	RNA linear PAT 17-AUG-2003
LOCUS	AR330124	
DEFINITION	Sequence	7526 from patent US 6566127.
ACCESSION	AR330124	
VERSION	AR330124.1	GI:33715932
KEYWORDS	Unknown.	
SOURCE	Unknown.	
ORGANISM	Unclassified.	
REFERENCE	1 (bases 1 to 38) Payco,P., Mcswiggen,J.A., Stinchcomb,D.T. and Escobedo,J. Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor Patent: US 6566127-A 7526 20-MAY-2003; Location/Qualifiers	
FEATURES source	1..38 /organism="unknown" /mol_type="unassigned RNA"	
ORIGIN		
Query Match	78.9%; Score 30;	DB 6;
Best Local Similarity	71.1%; Pred. NO. 0.053;	Length 38;
Matches	27; Conservative	6; Mismatches 5; Indels 0; Gaps 0;
Dy	<pre>1 CCUGCAAUCUGAUGAGCCGCGUAGGCCGAAAUCA 38 :: :: :: :: :: :: :: 1 CCTAAANTGTGATGAGCGCGTTAGCGCGAAATTCC 38</pre>	
RESULT 20		
AR330364	38 bp	RNA linear PAT 17-AUG-2003
LOCUS	AR330364	
DEFINITION	Sequence	7766 from patent US 6566127.
ACCESSION	AR330364	
VERSION	AR330364.1	GI:33716172
KEYWORDS	Unknown.	
SOURCE	Unknown.	
ORGANISM	Unclassified.	
REFERENCE	1 (bases 1 to 38) Payco,P., Mcswiggen,J.A., Stinchcomb,D.T. and Escobedo,J. Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor	

JOURNAL	Patent: US 6566127-A 7766 20-MAY-2003;
FEATURES	Location/Qualifiers
source	1..38 /organism="unknown" /mol_type="unassigned RNA"
ORIGIN	
Query Match	78.9%; Score 30; DB 6; Length 38;
Best Local Similarity	68.4%; Pred. No. 0.053;
Matches	26; Conservative 7; Mismatches 5; Indels 0; Gaps 0;
Oy	1 CCUGCAACUCGAGUAGGCCGCUUAGCCCGAAAAAACAAG 38 ::: : ::: :: 1 CCTGAATTCGTATGAGCGCCTTAGCGCGAAAACCTTCCG 38
Db	
RESULT 21	
LOCUS	ARJ32137 38 bp RNA linear PAT 17-AUG-2003
DEFINITION	Sequence 9539 from patent US 6566127.
ACCESSION	ARJ32137
VERSION	ARJ32137.1 GI:373717945
KEYWORDS	.
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	Unclassified. 1 (bases 1 to 38)
AUTHORS	Pavco, P., McSwigen, J.A., Stinchcomb, D.T. and Escobedo, J.
TITLE	Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor Patent: US 6566127-A 9539 20-MAY-2003;
JOURNAL	Location/Qualifiers
FEATURES	1..38 /organism="unknown" /mol_type="unassigned RNA"
source	
ORIGIN	
Query Match	78.9%; Score 30; DB 6; Length 38;
Best Local Similarity	83.3%; Pred. No. 0.053;
Matches	25; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
Oy	4 GCAAUCUGAUAGGCCGUUAGCCGAAAAA 33 ::: : ::: :: 4 GCATCTGATGAGCGCCTTAGCGCGAAAAA 33
Db	
RESULT 22	
LOCUS	AX227896 38 bp RNA linear PAT 10-SEP-2001
DEFINITION	Sequence 1268 from Patent WO0157206.
ACCESSION	AX227896
VERSION	AX227896.1 GI:15557037
KEYWORDS	.
SOURCE	synthetic construct
ORGANISM	synthetic construct
REFERENCE	other sequences; artificial sequences. 1
AUTHORS	Fatlaey, A.R., Jarvis, T., Mcswigen, J., Boher, R.N. and Holman, P.S.
TITLE	Method and reagent for the inhibition of checkpoint kinase-1 (chk 1) enzyme Patent: WO 0157206-A 1268 09-AUG-2001;
JOURNAL	RIBOZYME PHARMACEUTICALS, INC. (US) ; Fatlaey, Ali R. (US)
FEATURES	Location/Qualifiers
source	1..38 /organism="synthetic construct" /mol_type="unassigned RNA" /db_xref="taxon:32630"
ORIGIN	
Query Match	78.9%; Score 30; DB 6; Length 38;
Best Local Similarity	68.4%; Pred. No. 0.053;
Matches	26; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Qy	Db	RESULT 32	LOCUS	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES	ORIGIN
1	1	CCUGCAUCUGAUGAGCCGGUAGGCCGAAAAAUA	36											
1	1	CGTGAAGCTGATGAGCCGTTAGGCCGAAAGATCA	36											
2	2	CCUGCAUCUGAUGAGCCGGUAGGCCGAAAAAUA	37											
2	2	CTGAAGCTGATGAGCCGTTAGGCCGAAAGATCA	37											
3	3	CCUGCAUCUGAUGAGCCGGUAGGCCGAAAAAUA	38											
3	3	CTGAAGCTGATGAGCCGTTAGGCCGAAAGATCA	38											
4	4	CCUGCAUCUGAUGAGCCGGUAGGCCGAAAAAUA	39											
4	4	CTGAAGCTGATGAGCCGTTAGGCCGAAAGATCA	39											
5	5	CCUGCAUCUGAUGAGCCGGUAGGCCGAAAAAUA	40											
5	5	CTGAAGCTGATGAGCCGTTAGGCCGAAAGATCA	40											
6	6	CCUGCAUCUGAUGAGCCGGUAGGCCGAAAAAUA	41											
6	6	CTGAAGCTGATGAGCCGTTAGGCCGAAAGATCA	41											
7	7	CCUGCAUCUGAUGAGCCGGUAGGCCGAAAAAUA	42											
7	7	CTGAAGCTGATGAGCCGTTAGGCCGAAAGATCA	42											
8	8	CCUGCAUCUGAUGAGCCGGUAGGCCGAAAAAUA	43											
8	8	CTGAAGCTGATGAGCCGTTAGGCCGAAAGATCA	43											
9	9	CCUGCAUCUGAUGAGCCGGUAGGCCGAAAAAUA	44											
9	9	CTGAAGCTGATGAGCCGTTAGGCCGAAAGATCA	44											
10	10	CCUGCAUCUGAUGAGCCGGUAGGCCGAAAAAUA	45											
10	10	CTGAAGCTGATGAGCCGTTAGGCCGAAAGATCA	45											
11	11	CCUGCAUCUGAUGAGCCGGUAGGCCGAAAAAUA	46											
11	11	CTGAAGCTGATGAGCCGTTAGGCCGAAAGATCA	46											
12	12	CCUGCAUCUGAUGAGCCGGUAGGCCGAAAAAUA	47											
12	12	CTGAAGCTGATGAGCCGTTAGGCCGAAAGATCA	47											
13	13	CCUGCAUCUGAUGAGCCGGUAGGCCGAAAAAUA	48											
13	13	CTGAAGCTGATGAGCCGTTAGGCCGAAAGATCA	48											
14	14	CCUGCAUCUGAUGAGCCGGUAGGCCGAAAAAUA	49											
14	14	CTGAAGCTGATGAGCCGTTAGGCCGAAAGATCA	49											
15	15	CCUGCAUCUGAUGAGCCGGUAGGCCGAAAAAUA	50											
15	15	CTGAAGCTGATGAGCCGTTAGGCCGAAAGATCA	50											
16	16	CCUGCAUCUGAUGAGCCGGUAGGCCGAAAAAUA	51											
16	16	CTGAAGCTGATGAGCCGTTAGGCCGAAAGATCA	51											
17	17	CCUGCAUCUGAUGAGCCGGUAGGCCGAAAAAUA	52											
17	17	CTGAAGCTGATGAGCCGTTAGGCCGAAAGATCA	52											
18	18	CCUGCAUCUGAUGAGCCGGUAGGCCGAAAAAUA	53											
18	18	CTGAAGCTGATGAGCCGTTAGGCCGAAAGATCA	53											
19	19	CCUGCAUCUGAUGAGCCGGUAGGCCGAAAAAUA	54											

<hr/>					
<p>RESULT 34</p> <pre>AXZ19601 38 bp RNA linear PAT 07-SEP-2001 LOCUS AXZ19601 DEFINITION Sequence 5043 from Patent WO0159103. ACCESSION AXZ19601 VERSION AXZ19601.1 GI:15547325 KEYWORDS SOURCE . ORGANISM synthetic construct REFERENCE other sequences; artificial sequences.</pre>	<pre>Blatt,L., Mcswiggen,J. and Chowrira,B.M. Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression Patent: WO 0159103-A 5043 16-AUG-2001; RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ; McSwiggen, James (US) ; Chowrira, Bharat M. (US)</pre>				
ORIGIN	modified_base				
<hr/>					
<pre>Query Match 77.9%; Score 29.6; DB 6; Length 38; Best Local Similarity 70.3%; Pred. No. 0.08; Matches 26; Conservative 6; Mismatches 5; Indels 0; Gaps 0;</pre>	<pre>2 CTGCAUCUAGUAGCGCCGUUAGGCCGAANAUAUCAG 38 ::: : : : : : : : 2 CTTGTCTCCTGATGAGCGCGTTAGGCCCANAAATCAG 38</pre>				
<hr/>					
<p>RESULT 35</p> <pre>AXZ22613 38 bp RNA linear PAT 07-SEP-2001 LOCUS AXZ22613 DEFINITION Sequence 8055 from Patent WO0159103. ACCESSION AXZ22613 VERSION AXZ22613.1 GI:15550337 KEYWORDS SOURCE . ORGANISM synthetic construct REFERENCE other sequences; artificial sequences.</pre>	<pre>Blatt,L., Mcswiggen,J. and Chowrira,B.M. Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression Patent: WO 0159103-A 8055 16-AUG-2001; RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ; McSwiggen, James (US) ; Chowrira, Bharat M. (US)</pre>				
FEATURES	source				
<hr/>					
<p>ORIGIN</p> <pre>/organism="synthetic construct" /mol_type="unassigned RNA" /db_xref="taxon:32630" /note="Nucleic Acid"</pre>					
<hr/>					
<p>ORIGIN</p> <pre>Query Match 77.9%; Score 29.6; DB 6; Length 38; Best Local Similarity 72.2%; Pred. No. 0.08; Matches 26; Conservative 6; Mismatches 4; Indels 0; Gaps 0;</pre>	<pre>3 UGCaucuagAUGCgCcGuUAgGcCcGaAAAAAuCaG 38 .: .:. .:. .:. .:. .:. .:. .:. .:. . 3 TGAATCTGAtGAGtGGccGttAgGccGAaaaaaaAAg 38</pre>				
<hr/>					
RESULT 36					
<hr/>					

LOCUS	AX227899	38 bp	RNA	linear	PAT 10-SEP-2003
DEFINITION	Sequence 1271 from Patent WO0157206.				
ACCESSION	AX227899				
VERSION	AX227899.1				
KEYWORDS	GI:15557040				
SOURCE					
ORGANISM	synthetic construct				
REFERENCE	other sequences; artificial sequences.				
AUTHORS	1 Pattaey,A.R., Jarvis,T., Mcswiggen,J., Booher,R.N. and Holman,P.S.				
TITLE	Method and reagent for the inhibition of checkpoint kinase-1 (chk 1) enzyme				
JOURNAL	Patent: WO 0157206-A 1271 09-AUG-2001;				
FEATURES	RIBOZYME PHARMACEUTICALS, INC. (US) ; Pattaey, Ali R. (US)				
source	Location/Qualifiers				
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	/mol_type="unassigned RNA"				
	/db_xref="taxon:32630"				
ORIGIN					
Query Match	77.9%; Score 29.6; DB 6; Length 38;				
Best Local Similarity	75.0%; Pred.No.0.08;				
Matches	27; Conservative 5; Mismatches 4; Indels 0; Gaps 0;				
QY	1 CCUGCAUCUGAUGAGCCGCUUAGCCGAAAUAUCA 36				
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Db	1 CATGCAGACTGATGAGCCGTTAGCCGAAAACCA 36				
	: : : : : : : : : : : : : : : :				
RESULT 37					
LOCUS	AX580764	38 bp	RNA	linear	PAT 10-JAN-2003
DEFINITION	Sequence 2602 from Patent WO0211674.				
ACCESSION	AX580764				
VERSION	AX580764.1				
KEYWORDS	GI:27649966				
SOURCE					
ORGANISM	synthetic construct				
REFERENCE	synthetic construct				
AUTHORS	other sequences; artificial sequences.				
TITLE	1 Thompson,J., Mcswiggen,J., McKenzie,T., Ayers,D., Szymkowski,D.B.				
JOURNAL	and Grube,A. Method and reagent for the inhibition of calcium activated chloride channel-1 (clca-1)				
	Patent: WO 0211674-A 2602 14-FEB-2002;				
	RIBOZYME PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ;				
	Thompson, James (US)				
FEATURES	Location/Qualifiers				
source	1..38				
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	/note="Enzymatic Nucleic Acid"				
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RESULT 38					
LOCUS	AX580873	38 bp	RNA	linear	PAT 10-JAN-2003
DEFINITION	Sequence 2711 from Patent WO0211674.				
ACCESSION	AX580873				
VERSION	AX580873.1				
KEYWORDS	GI:27650075				
SOURCE	synthetic construct				

ORGANISM	synthetic construct other sequences; artificial sequences.						
REFERENCE	1 Thompson,J., Mcswiggen,J., McKenzie,T., Ayers,D., Szymkowski,D.E. and Grube,A. Method and reagent for the inhibition of calcium activated chloride channel-1 (Clca-1)						
JOURNAL	PATENT: WO 021674-A 2711 14-FEB-2002; RHOZATWE PHARMACEUTICALS, INC. (US) ; Syntex (U.S.A.) LLC (US) ; Thompson, James (US) Location/Qualifiers						
FEATURES	source 1..38 /organism="synthetic construct" /mol_type="unassigned RNA" /db_xref="taxon:32630" /note="Enzymatic Nucleic Acid"						
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Query Match	77.9%;	Score 29.6;	DB 6;	Length 38;			
Best Local Similarity	72.2%;	Pred.No. 0.08;					
Matches	26;	Conservative 6;	Mismatches 4;	Indels 0;	Gaps 0;		
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Db							
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ARJ30254	ARJ30254		38 bp	RNA	linear	PAT 17-AUG-2003	
LOCUS							
DEFINITION	Sequence 7656 from patent US 6566127.						
ACCESSION	ARJ30254.1						
VERSION	ARJ30254.1 GI:33716062						
KEYWORDS	Unknown. Unclassified.						
SOURCE							
ORGANISM	Unclassified.						
REFERENCE	1 (bases 1 to 38) Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J. Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor Patent: US 6566127-A 7656 20-MAY-2003; Location/Qualifiers						
JOURNAL	1..38 /organism="unknown" /mol_type="unassigned RNA"						
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source							
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RESULT 40							
ARJ30461	ARJ30461		38 bp	RNA	linear	PAT 17-AUG-2003	
LOCUS							
DEFINITION	Sequence 7863 from patent US 6566127.						
ACCESSION	ARJ30461						
VERSION	ARJ30461.1 GI:33716269						
KEYWORDS							
SOURCE	Unknown. Unknowm. Unclassified.						
ORGANISM							
REFERENCE	1 (bases 1 to 38) Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J. Method and reagent for the treatment of diseases or conditions related to levels of vascular endothelial growth factor receptor Patent: US 6566127-A 7863 20-MAY-2003; Location/Qualifiers						
JOURNAL							
FEATURES							

source 1.38
/organism="unknown"
/mol_type="unassigned RNA"
ORIGIN

Query Match 77.4%; Score 29.4; DB 6; Length 38;
Best Local Similarity 80.6%; Pred. No. 0.098;
Matches 25; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
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Db 6 AAACGATGAGCGCCGTTAGGCCGAAAUCA 36

Search completed: May 13, 2005, 18:17:11
Job time : 1091.95 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using bw model

Run on: May 13, 2005, 16:40:53 ; Search time 275.673 Seconds
(without alignments)
816.004 Million cell updates/sec

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Perfect score: 38
Sequence: 1 ccgcaucugaugagcgccguuagcgcaaaaacag 38

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 4530610

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

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4: geneseqn2001a:*
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6: geneseqn2002a:*
7: geneseqn2002a:*
8: geneseqn2003a:*
9: geneseqn2003a:*
10: geneseqn2003a:*
11: geneseqn2004a:*
12: geneseqn2004a:*
13: geneseqn2004a:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	38	100.0	38	6	ABK57961	Abk57961 Human CLC
2	36	94.7	36	6	ABK61061	Abk61061 Human CLC
3	31.8	83.7	38	4	ABK04137	Abk04137 Human NOG
4	31.4	82.6	38	4	ABK04336	Abk04336 Human NOG
5	31.4	82.6	38	4	ABK47321	Abk47321 Human GR1
6	31.4	82.6	38	6	ABK57933	Abk57933 Human CLC
7	31.4	82.6	38	8	ACD52864	Acid52864 HBV Inozoy
8	31.4	82.6	38	11	ADM54641	Adm54641 Hammethea
9	31.4	82.6	38	12	ADM61662	Adm61662 Hepatitis
10	31.2	82.1	38	6	ACN26747	Acn26747 WNV minus
11	31.2	82.1	38	6	ACN27300	Acn27300 WNV minus
12	30.8	81.1	38	6	ACN26250	Acn26250 WNV minus
13	30.6	80.5	38	6	ACN26622	Acn26622 WNV minus
14	30.6	80.5	38	6	ACN27117	Acn27117 WNV minus
15	30.6	80.5	38	11	ADL55912	Adl55912 Human PKR
16	30.4	80.0	38	4	ABK07829	Abk07829 Human CD2
17	30.4	80.0	38	4	ABK05084	Abk05084 Human NOG
18	30.4	80.0	38	4	ABK04387	Abk04387 Human NOG
19	30.4	80.0	38	6	ACN29362	Acn29362 WNV minus
20	30.2	79.5	38	4	ABK04516	Abk04516 Human NOG

21	30.2	79.5	38	6	ACN26549	Acn26549 WNV minus
22	30.2	79.5	38	6	ACN30394	Acn30394 WNV minus
23	30	78.9	38	4	AAH96054	Aah96054 Human Chk
24	30	78.9	38	6	ABK58289	Abk58289 Human CLC
25	30	78.9	38	6	ACN26440	Acn26440 WNV minus
26	30	78.9	38	6	ACN26144	Acn26144 WNV minus
27	30	78.9	38	8	ACD50521	Acid50521 HBV Hamme
28	30	78.9	38	11	ADL53551	Adl53551 Human IKK
29	30	78.9	38	11	ADL55719	Adl55719 Human PKR
30	30	78.9	38	12	ADM60497	Adm60497 Hepatitis
31	29.8	78.4	38	4	ABK07861	Abk07861 Human CD2
32	29.8	78.4	38	4	ABK04290	Abk04290 Human NOG
33	29.8	78.4	38	4	ABK04122	Abk04122 Human NOG
34	29.8	78.4	38	4	ABK05109	Abk05109 Human NOG
35	29.8	78.4	38	6	ACN26108	Acn26108 WNV minus
36	29.8	78.4	38	6	ACN27859	Acn27859 WNV minus
37	29.8	78.4	38	8	ACD50588	Acid50588 HBV Hamme
38	29.8	78.4	38	11	ADL56345	Adl56345 Human PKR
39	29.8	78.4	38	12	ADM60513	Adm60513 Hepatitis
40	29.6	77.9	36	6	ABX02648	Abx02648 HCV Hamme
41	29.6	77.9	38	4	AAH96057	Aah96057 Human Chk
42	29.6	77.9	38	4	ABK08055	Abk08055 Human CD2
43	29.6	77.9	38	4	ABK04315	Abk04315 Human NOG
44	29.6	77.9	38	4	ABK04156	Abk04156 Human NOG
45	29.6	77.9	38	4	ABK05043	Abk05043 Human NOG
46	29.6	77.9	38	6	ABK58231	Abk58231 Human CLC
47	29.6	77.9	38	6	ABK58340	Abk58340 Human CLC
48	29.6	77.9	38	6	ACN15841	Acn15841 WNV Hamme
49	29.6	77.9	38	6	ACN15568	Acn15568 WNV Hamme
50	29.6	77.9	38	6	ACN26805	Acn26805 WNV minus
51	29.6	77.9	38	8	ACA07297	ACA07297 Nectofis
52	29.6	77.9	38	11	ADL75131	Adl75131 Human PTG
53	29.6	77.9	38	11	ADL55642	Adl55642 Human PKR
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55	29.6	77.9	38	11	ADL53910	Adl53910 Human IKK
56	29.4	77.4	38	6	ABK05016	Abk05016 Human NOG
57	29.4	77.4	38	6	ABK19488	Abk19488 Human ERG
58	29.4	77.4	38	6	ABK58570	Abk58570 Human CLC
59	29.4	77.4	38	6	ACN15685	Acn15685 WNV Hamme
60	29.4	77.4	38	6	ACN29834	Acn29834 WNV minus
61	29.4	77.4	38	8	ACD50819	Acid50819 HBV Hamme
62	29.4	77.4	38	11	ADL56415	Adl56415 Human PKR
63	29.4	77.4	38	11	ADL55806	Adl55806 Human PKR
64	29.4	77.4	38	12	ADM60642	Adm60642 Hepatitis
65	29.2	76.8	38	4	AAH96523	Aah96523 Human Chk
66	29.2	76.8	38	4	AAH96098	Aah96098 Human Chk
67	29.2	76.8	38	4	ABK04404	Abk04404 Human NOG
68	29.2	76.8	38	4	ABK07816	Abk07816 Human CD2
69	29.2	76.8	38	4	ABK04146	Abk04146 Human NOG
70	29.2	76.8	38	4	ABK07920	Abk07920 Human CD2
71	29.2	76.8	38	4	ABK04178	Abk04178 Human NOG
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73	29.2	76.8	38	6	ACN27849	Acn27849 WNV minus
74	29.2	76.8	38	6	ACN28525	Acn28525 WNV minus
75	29.2	76.8	38	6	ACN18013	Acn18013 WNV Inozoy
76	29.2	76.8	38	6	ACN16341	Acn16341 WNV Hamme
77	29.2	76.8	38	8	ACD51196	Acid51196 HBV Hamme
78	29.2	76.8	38	11	ADL56115	Adl56115 Human PKR
79	29.2	76.8	38	12	ADM60815	Adm60815 Hepatitis
80	29	76.3	38	4	ABK04409	Abk04409 Human NOG
81	29	76.3	38	4	ABK04223	Abk04223 Human NOG
82	29	76.3	38	6	ABK04040	Abk04040 Human NOG
83	29	76.3	38	6	ABK19554	Abk19554 Human ERG
84	29	76.3	38	6	ABK19868	Abk19868 Human ERG
85	29	76.3	38	6	ABK58056	Abk58056 Human CLC
86	29	76.3	38	6	ACN27000	Acn27000 WNV minus
87	29	76.3	38	6	ACN15353	Acn15353 WNV Hamme
88	29	76.3	38	6	ACN15684	Acn15684 WNV Hamme
89	29	76.3	38	6	ACN26650	Acn26650 WNV minus
90	29	76.3	38	6	ACN15708	Acn15708 WNV Hamme
91	29	76.3	38	6	ACN16624	Acn16624 WNV Hamme
92	29	76.3	38	6	ACN17952	Acn17952 WNV Inozoy
93	28.8	75.8	36	6	ABX03069	Abx03069 HCV Hamme

94	28.8	75.8	38	4	AAH96035	Aahb6035	Human	Chk
95	28.8	75.8	38	4	AAH96344	Aahb6344	Human	Chk
96	28.8	75.8	38	4	AAH96309	Aahb6309	Human	Chk
97	28.8	75.8	38	4	ABK04054	ABK04054	Human	NOG
98	28.8	75.8	38	4	ABK04058	ABK04058	Human	NOG
99	28.8	75.8	38	4	ABK07775	ABK07775	Human	CD2
100	28.8	75.8	38	4	ABK04144	ABK04144	Human	NOG

ALIGNMENTS

RESULT 1
 ID ABRK57961 standard; RNA; 38 BP.
 AC ABRK57961;
 DT 02-JUL-2002 (first entry)
 DE Human CLCA1 gene enzymatic nucleic acid #2332.
 XX Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;
 XX antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;
 XX chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;
 XX oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic
 XX acetylcholine.
 OS Homo sapiens.
 PN WO200211674-A2.
 XX
 PD 14-FEB-2002.
 XX
 PF 09-AUG-2001; 2001WO-US024970.
 XX
 PR 09-AUG-2000; 2000US-0224383P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (SYNT) SYNTEx USA LLC.
 PA (THOM/) THOMPSON J.
 XX
 PI Thompson J, Mcswiggen J, McKenzie T, Ayers D, Szymkowski DE;
 PI Gruppe A;
 DR WPI; 2002-217145/27.
 PT Enzymatic polynucleotide that down regulates expression of chloride
 PT channel calcium activated gene, useful for treating Chronic obstructive
 PT pulmonary disease (COPD), chronic bronchitis and asthma.
 PS
 XX
 PS Claim 5; Page 55; 152pp; English.
 CC The invention relates to enzymatic nucleic acid molecules that down
 CC regulate expression of chloride channel calcium activated 1 (CLCA1) genes
 CC by cleaving RNA derived from the genes. The nucleic acid sequences are
 CC useful as pharmaceutical agents for treating conditions such as chronic
 CC obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic
 CC fibrosis, obstructive bowel syndrome and any other diseases or condition
 CC that are related to or will respond to the levels of CLCA1 in a cell or
 CC tissue. The sequences are useful for reducing CLCA1 activity in a cell,
 CC hence, are useful for treatment of a patient having a condition
 CC associated with the level of CLCA1, where the invention further comprises
 CC the use of one or more therapies under conditions suitable for the
 CC treatment, for example, oxygen therapy, bronchodilators, corticosteroids
 CC antibacterials, vaccinations, acetylcholine and mucokinetic agents. The
 CC nucleic acids of the invention are also used as diagnostic tools to
 CC examine genetic drift and mutations in diseased cells or to detect
 CC the presence of CLCA1 RNA in a cell. This sequence represents an
 CC enzymatic nucleic acid molecule of the invention
 XX
 XX Sequence 38 BP; 11 A; 9 C; 11 G; 0 T; 7 U; 0 Other;

Query Match	100.0%	Score 38	DB 6	Length 38
Best Local Similarity	100.0%	Pred. No.	7.7e-07	
Matches 38	Conservative 0	Mismatches 0	Indels 0	Gaps 0
Qy	1	CTUCGCAUUCGAGUGAGGCCGUTUAGCCGAAAAUACAG	38	
Db	1	CTUCGCAUUCGAGUGAGGCCGUTUAGCCGAAAAUACAG	38	

RESULT 2

QY 2 CUGCAUUCUGAUGAGCCGUGAGCCGAAAAUACAG 37
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 DB 1 CUGCAUUCUGAUGAGCCGUGAGCCGAAAAUACAG 36

RESULT 3

ABK04137
 ID ABK04137 standard; RNA; 38 BP.

XX ABK04137;

DT 12-MAR-2002 (first entry)

XX Human NOGO Hammerhead ribozyme substrate sequence #344.

XX Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
 KM cerebroprotective; neurotrophic; neuroprotective; antiparkinsonian;
 KM muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
 KM DNazyme; inozyme; G-cleaver; ambezyme; zinzyme; lymphoma; leukaemia;
 KM B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
 KM human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
 KM MCL; immunocytoma; IMC; immune thrombocytopenia; stroke; dementia;
 KM inflammatory arthropathy; central nervous system injury;
 KM cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
 KM chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
 KM Parkinson's disease; ataxia; Huntington's disease; substrate sequence;
 KM Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.

XX Homo sapiens.
 OS Synthetic.

XX MO200159103-A2.

XX 16-AUG-2001.

XX 09-FEB-2001; 2001WO-US004273.

XX 11-FEB-2000; 2000US-0181797P.

XX 28-FEB-2000; 2000US-0185516P.

XX 06-MAR-2000; 2000US-0187128P.

XX (RIBO-) RIBOZYME PHARM INC.

XX (BLAT/) BLATT L.

XX (MCSW/) MCSWIGGEN J.

XX (CHOW/) CHOWRIRA B M.

XX Blatt L, Mcswiggen J, Chowrira BM;

XX MPI; 2001-607195/69.

XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense

XX constructs, which down regulate expression of a CD20 gene or neurite

XX growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and

XX central nervous system injury.

XX Claim 89; Page 71; 200pp; English.

XX The invention relates to a nucleic acid molecule which down regulates
 CC expression of a CD20 gene and a nucleic acid molecule which down
 CC regulates expression of a neurite growth inhibitor gene (NOGO). The
 CC nucleic acids may be enzymatic nucleic acids (e.g., a ribozyme or a
 CC DNazyme) an inozyme (an endolytic nucleic acid cleaving an RNA molecule
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) or
 CC an ambezyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA
 CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA
 CC of CD20 in the presence of a divalent cation that is preferably Mg²⁺.
 CC Furthermore, it may be contacted with a cell to reduce CD20 activity of
 CC the cell and treat a patient having a condition associated with the level
 CC of CD20. The treatment may further comprise the use of one or more
 CC therapies. In particular, the CD20 targeting nucleic acid may be used to
 CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic

CC Leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
 CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
 CC immune thrombocytopenia, and inflammatory arthropathy. The NOGO-
 CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the
 CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the
 CC nucleic acid may be contacted with a cell to reduce NOGO activity of the
 CC cell and treat a patient having a condition associated with the level of
 CC NOGO. The treatment may further comprise the use of one or more
 CC therapies. In particular, the NOGO-targeting nucleic acid may be used to
 CC treat central nervous system (CNS) injury and cerebrovascular accident
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
 CC disease, muscular dystrophy, and/or other neurodegenerative disease
 CC states which respond to the modulation of NOGO expression. The present
 CC sequence is a substrate sequence for a nucleic acid of the invention
 CC based on the human NOGO sequence

XX Sequence 38 BP; 12 A; 8 C; 8 G; 0 T; 10 U; 0 Other;

XX Query Match 83.7%; Score 31.8; DB 4; Length 38;

XX Best Local Similarity 94.3%; Pred. No. 0.00042;

XX Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CUGCAUUCUGAUGAGCCGUGAGCCGAAAAUACAG 36
 |||||
 DB 2 CUUUAUUCUGAUGAGCCGUGAGCCGAAAAUACAG 36

XX RESULT 4
 XX ABK04336
 XX ID ABK04336 standard; RNA; 38 BP.

XX ABK04336;

XX 12-MAR-2002 (first entry)

XX Human NOGO Hammerhead ribozyme substrate sequence #543.

XX Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
 KM cerebroprotective; neurotrophic; neuroprotective; antiparkinsonian;
 KM muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
 KM DNazyme; inozyme; G-cleaver; ambezyme; zinzyme; lymphoma; leukaemia;
 KM B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
 KM human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
 KM MCL; immunocytoma; IMC; immune thrombocytopenia; stroke; dementia;
 KM inflammatory arthropathy; central nervous system injury;
 KM cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
 KM chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
 KM Parkinson's disease; ataxia; Huntington's disease; substrate sequence;
 KM Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.

XX Homo sapiens.
 OS Synthetic.

XX MO200159103-A2.

XX 16-AUG-2001.

XX 09-FEB-2001; 2001WO-US004273.

XX 11-FEB-2000; 2000US-0181797P.

XX 28-FEB-2000; 2000US-0185516P.

XX 06-MAR-2000; 2000US-0187128P.

XX (RIBO-) RIBOZYME PHARM INC.

XX (BLAT/) BLATT L.

XX (MCSW/) MCSWIGGEN J.

XX (CHOW/) CHOWRIRA B M.

XX Blatt L, Mcswiggen J, Chowrira BM;

XX MPI; 2001-607195/69.

XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
PT constructs, which down regulate expression of a CD20 gene or neurite
PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
PT central nervous system injury.
XX
PS Claim 89; Page 74; 200pp; English.
XX
CC The invention relates to a nucleic acid molecule which down regulates
CC expression of a CD20 gene and a nucleic acid molecule which down
CC regulates expression of a neurite growth inhibitor gene (NOCO). The
CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
CC DNAzyme) an Inozyme (an endolytic nucleic acid cleaving an RNA molecule
CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) or
CC an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA
CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA
CC of CD20 in the presence of a divalent cation that is preferably Mg^{2+} .
CC Furthermore, it may be contacted with a cell to reduce CD20 activity of
CC the cell and treat a patient having a condition associated with the level
CC of CD20. The treatment may further comprise the use of one or more
CC therapies. In particular, the CD20-targeting nucleic acid may be used to
CC treat lymphoma, leukemia, B-cell lymphoma, low-grade or follicular non-
CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, mantle-cell
CC leukemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
CC immune thrombocytopenia, and inflammatory arthropathy. The NOCO-
CC targeting nucleic acid is used to cleave RNA of the NOCO gene in the
CC presence of a divalent cation that is preferably Mg^{2+} . Furthermore, the
CC nucleic acid may be contacted with a cell to reduce NOCO activity of the
CC cell and treat a patient having a condition associated with the level of
CC NOCO. The treatment may further comprise the use of one or more
CC therapies. In particular, the NOCO-targeting nucleic acid may be used to
CC treat central nervous system (CNS) injury and cerebrovascular accident
CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
CC disease, muscular dystrophy, and/or other neurodegenerative disease
CC states which respond to the modulation of NOCO expression. The present
CC sequence is a substrate sequence for a nucleic acid of the invention
CC based on the human NOCO sequence
XX
SQ Sequence 38 BP; 11 A; 9 C; 11 G; 0 T; 7 U; 0 Other;
XX
Query Match 82.6%; Score 31.4; DB 4; Length 38;
Best Local Similarity 97.0%; Pred. No. 0.00063;
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 5 CAUUCUGAUGAGCGCGUUGAGCCGAAAAAUCAG 37
DB |||||
5 CAUUCUGAUGAGCGCGUUGAGCCGAAAAAUCAG 37
XX
RESULT 5
ABL47321
ID ABL47321 standard; RNA; 38 BP.
XX
AC ABL47321;
XX
DT 27-JUN-2003 (first entry)
XX
DE Human GRID hammerhead ribozyme oligonucleotide #49.
XX
XX Human; Grb2-related with Insert Domain; GRID; T-cell; ribozyme;
KM co-stimulatory adaptor protein; tissue rejection; graft rejection;
KW leukemia; cytosolic; ss.
XX
OS Homo sapiens.
XX
XX WO200162911-A2.
FN
XX 30-AUG-2001.
PD
XX 23-FEB-2001; 2001WO-US005957.
PF

XX
PR 24-FEB-2000; 2000US-0184594P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA (GLAX) GLAXO GROUP LTD.
XX
XX Jarvis T, Von Carlowitz I, Mcswiggen JA, Hamblin PA, Ellis JH;
PI
XX MPI; 2001-550088/61.
DR
XX
PT New nucleic acid(s) for regulating the Grb2-related with Insert Domain
PT (GRID) gene comprises using antisense and enzymatic nucleic acid
PT molecules such as hammerhead ribozymes.
XX
PS Claim 5; Page 60; 108pp; English.
XX
CC The present invention relates to oligonucleotides that downregulate the
CC expression of human Grb2-related with Insert Domain (GRID) gene. GRID is
CC a T-cell co-stimulatory adaptor protein. The oligonucleotides are useful
CC for modulating the expression of GRID, to treat conditions such as
CC tissue/graft rejection and leukemia. The oligonucleotides can also be
CC administered in conjunction with other therapies such as radiation,
CC chemotherapy and cyclosporin treatment. The present oligonucleotide was
CC used to illustrate the invention
XX
SQ Sequence 38 BP; 14 A; 7 C; 11 G; 0 T; 6 U; 0 Other;
XX
Query Match 82.6%; Score 31.4; DB 4; Length 38;
Best Local Similarity 97.0%; Pred. No. 0.00063;
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 4 GCAUUCUGAUGAGCGCGUUGAGCCGAAAAAUC A 36
DB |||||
4 GCAUUCUGAUGAGCGCGUUGAGCCGAAAAAUC A 36
XX
RESULT 6
ABK57933
ID ABK57933 standard; RNA; 38 BP.
XX
AC ABK57933;
XX
DT 02-JUL-2002 (first entry)
XX
DE Human CLCA1 gene enzymatic nucleic acid #2304.
XX
XX Human; chloride channel calcium activated 1; CLCA1; ss; antiasthmatic;
KM antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;
KW chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;
KW oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;
acetylcysteine.
XX
OS Homo sapiens.
XX
XX WO200211674-A2.
FN
XX 14-FEB-2002.
PD
XX 09-AUG-2001; 2001WO-US024970.
PF
XX 09-AUG-2000; 2000US-0224383P.
PR
XX (RIBO-) RIBOZYME PHARM INC.
PA (SYNT) SYNTEX USA LLC.
PA (THOM/) THOMPSON J.
XX
XX Thompson J, Mcswiggen J, McKenzie T, Ayers D, Szymkowski DE;
PI Grube A;
XX WPI; 2002-217145/27.
DR
XX
PT Enzymatic polynucleotide that down regulates expression of chloride
PT channel calcium activated gene, useful for treating Chronic obstructive

PT pulmonary disease (COPD), chronic bronchitis and asthma.
XX
PS Claim 5; Page 55; 152pp; English.
XX
CC The invention relates to enzymatic nucleic acid molecules that down
CC regulate expression of chloride channel calcium activated 1 (ClCA1) genes
CC by cleaving RNA derived from the genes. The nucleic acid sequences are
CC useful as pharmaceutical agents for treating conditions such as chronic
CC obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic
CC fibrosis, obstructive bowel syndrome and any other diseases or conditions
CC that are related to or will respond to the levels of ClCA1 in a cell or
CC tissue. The sequences are useful for reducing ClCA1 activity in a cell,
CC hence, are useful for treatment of a patient having a condition
CC associated with the level of ClCA1, where the invention further comprises
CC the use of one or more therapies under conditions suitable for the
CC treatment, for example, oxygen therapy, bronchodilators, corticosteroids,
CC antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The
CC nucleic acids of the invention are also used as diagnostic tools to
CC examine genetic drift and mutations within diseased cells or to detect
CC the presence of ClCA1 RNA in a cell. This sequence represents an
CC enzymatic nucleic acid molecule of the invention
CC
XX
SQ Sequence 38 BP; 11 A; 7 C; 10 G; 0 T; 10 U; 0 Other;
Query Match 82.6%; Score 31.4; DB 6; Length 38;
Best Local Similarity 97.0%; Pred. No. 0.00063;
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3 UGCAUUCUGAUGAGCGCCGUUAGCCGGAANAUC 35
Db 3 UGAAAUUCUGAUGAGCGCCGUUAGCCGGAANAUC 35
RESULT 7
ACDS2864
ID ACDS2864 standard; RNA; 38 BP.
XX
AC ACDS2864;
XX
XX 24-SEP-2003 (first entry)
DT
XX
DE HBV inozyme sequence #586.
XX
XX Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
XX RNA stability; RNA expression; RNA synthesis; antisense;
XX enzymatic nucleic acid; hammerhead ribozyme; DNazyme; inozyme; zinzyme;
XX amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;
XX HBV reverse transcriptase; Enhancer 1 region; viral replication;
XX degenerative; disease state; HBV infection; HCV infection; cirrhosis;
XX liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
XX vincristine; antiinflammatory; ss.
XX
XX Hepatitis B virus.
OS
XX
PN WO200281494-A1.
XX
PD 17-OCT-2002.
XX
XX 26-MAR-2002; 2002WO-US009187.
PF
XX
XX 26-MAR-2001; 2001US-00817879.
PR
XX 08-JUN-2001; 2001US-00877478.
PR
XX 08-JUN-2001; 2001US-0296876P.
PR
XX 24-OCT-2001; 2001US-0335059P.
PR
XX 05-DEC-2001; 2001US-0337055P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLAT L.
PA (MAGE/) MAGEJAK D.
PA (MCSW/) MCSWIGGEN J.
PA (MORR/) MORRISSEY D.
PA (PAVC/) PAVCO P.
PA (LEE/) LEE P.

PA (DRAE/) DRAPER K.
PA (ROBE/) ROBERTS E.
XX
XX Blate L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;
PI Draper K, Roberts E;
XX WPI, 2003-229207/22.
DR
XX
XX Novel compound useful for treating cirrhosis, liver failure,
PT hepatocellular carcinoma, or condition associated with hepatitis C virus
PT infection.
XX
XX Example 1; Page 161; 387pp; English.
PS
XX
XX The present invention relates to nucleic acid molecules which modulate
CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,
CC inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed
CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse
CC transcriptase and/or HBV reverse transcriptase primer sequences, as well
CC as oligonucleotides that specifically bind the Enhancer 1 region of HBV
CC DNA. The nucleic acids may be used to modulate the expression of HBV
CC genes and HBV viral replication. Also disclosed is a method for screening
CC compounds and/or potential therapies directed against HBV, and compounds
CC that modulate the expression and/or replication of HCV. The compounds and
CC methods of the invention are useful for the treatment of degenerative and
CC disease states related to HBV and HCV infection, replication and gene
CC expression such as cirrhosis, liver failure, and hepatocellular
CC carcinoma. The present sequence represents one of the HBV ribozyme,
CC inozyme, G-cleaver, zinzyme, DNazyme or amberzyme sequences disclosed in
CC the present invention
CC
XX
SQ Sequence 38 BP; 11 A; 9 C; 10 G; 0 T; 7 U; 1 Other;
Query Match 82.6%; Score 31.4; DB 8; Length 38;
Best Local Similarity 94.1%; Pred. No. 0.00063;
Matches 32; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 CCUGCAUUCUGAUGAGCGCCGUUAGCCGGAANAUC 34
Db 1 CCUGCAUUCUGAUGAGCGCCGUUAGCCGGAANAUC 34
RESULT 8
ADMS4641
ID ADMS4641 standard; RNA; 38 BP.
XX
XX ADMS4641;
XX
XX 03-JUN-2004 (first entry)
DT
XX
XX Hammerhead ribozyme targeting human GRID #49.
DE
XX
XX Human; ss; GRID; Grid2-related with insert domain; hammerhead ribozyme;
XX NCH ribozyme; G-cleaver ribozyme; zinzyme; DNazyme; amberzyme; Inozyme;
XX hairpin ribozyme; tissue rejection; graft rejection; leukaemia.
XX
XX Homo sapiens.
OS
XX Synthetic.
OS
XX
PN US2003134806-A1.
XX
XX 17-UTL-2003.
PD
XX
XX 23-FEB-2001; 2001US-00792818.
PF
XX
XX 10-FEB-2000; 2000US-0181594P.
PR
XX
XX (JARV/) JARVIS T.
PA (CARL/) CARLOWITZ I V.
PA (MCSW/) MCSWIGGEN J.
PA (HAMB/) HAMBELIN P A.

PA (BLU/) ELLIS J. H.
 PI Jarvis T, Carlowitz IV, Mcswiggen J, Hamblin PA, Ellis JH;
 XX WPI; 2003-829646/77.
 DR
 XX
 PT New nucleic acid molecule that down-regulates expression of Gb2-related
 PT with insert domain (GRID) gene, useful for treating a condition
 PT associated with the level of GRID, e.g. tissue/graft rejection and
 PT leukemia.
 PS Claim 5; SEQ ID NO 954; 74bp; English.
 XX
 CC The invention relates to a nucleic acid molecule that down-regulates
 CC expression of Gb2-related with insert domain (GRID) gene, e.g. a
 CC hammerhead ribozyme, NCH ribozyme, G-cleaver ribozyme, Zinzyme, DNzyme,
 CC amberzyme, inozyme or hairpin ribozyme. Also include are a mammalian cell
 CC including the novel nucleic acid molecule, reducing GRID activity in a
 CC cell by contacting the cell with the novel nucleic acid molecule,
 CC creating a patient having a condition associated with the level of GRID
 CC (e.g. tissue/graft rejection or leukemia) by contacting the cell with
 CC the novel nucleic acid molecule, cleaving RNA of a GRID gene by
 CC contacting the cell with the novel nucleic acid molecule, an expression
 CC vector comprising a nucleic acid sequence (encoding at least the novel
 CC nucleic acid molecule in a manner that allows its expression), a
 CC mammalian cell including the expression vector and an enzymatic nucleic
 CC acid molecule that cleaves RNA derived from a GRID gene. The nucleic acid
 CC molecule is useful for treating a condition associated with the level of
 CC GRID, e.g. tissue/graft rejection and leukemia. The present sequence is
 CC a hammerhead ribozyme of the invention.
 CC
 SQ Sequence 38 BP; 14 A; 7 C; 11 G; 0 T; 6 U; 0 Other;
 Query Match 82.6%; Score 31.4; DB 11; Length 38;
 Best Local Similarity 97.0%; Pred. No. 0.00063;
 Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 4 GCAUUCGAGUAGGCCGUGAGCCGAAAAUUA 36
 DB 4 GCAGUCUGAGAGCCGUGUAGCCGAAAAUUA 36
 RESULT 9
 ADM61662
 ID ADM61662 standard; RNA; 38 BP.
 AC ADM61662;
 XX
 DT 03-JUN-2004 (first entry)
 DE Hepatitis B virus (HBV) enzymatic nucleic acid #1254.
 XX
 KW Hepatitis B virus; HBV; ss; enzymatic nucleic acid; RNA cleavage;
 KW hepatitis B virus infection; hepatitis; hepatocellular carcinoma;
 KW cirrhosis; liver failure; lamivudine; interferon; genetic drift;
 KW vironcide; hepatocytic; antiinflammatory; cytoskeletal.
 XX
 OS Hepatitis B virus.
 XX
 PN US2004054156-A1.
 XX
 PD 18-MAR-2004.
 XX
 PF 15-JAN-2003; 2003US-00342902.
 XX
 PR 14-MAY-1992; 92US-00882712.
 PR 07-FEB-1994; 94US-00193627.
 PR 08-NOV-1999; 99US-00436430.
 PR 20-MAR-2000; 2000US-00531025.
 PR 09-AUG-2000; 2000US-00636385.
 PR 24-OCT-2000; 2000US-00696347.
 PR 08-JUN-2001; 2001US-00877478.
 XX

PA (DRAP/) DRAPER K.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J A.
 PA (MORR/) MORRISSEY D.
 XX
 PI Draper K, Blatt L, Mcswiggen JA, Morrissey D;
 XX WPI; 2004-247781/23.
 DR
 XX
 PT Novel enzymatic nucleic acid molecule such as DNzymes and inozymes
 PT specifically cleaving RNA derived from hepatitis B virus and comprising
 PT one or more binding arms, useful for treating hepatitis and cirrhosis.
 PS Disclosure; SEQ ID NO 3796; 122bp; English.
 XX
 CC The invention relates to an enzymatic nucleic acid molecule that
 CC specifically cleaves RNA derived from hepatitis B virus (HBV) and
 CC comprising one or more binding arms, without requiring the presence of a
 CC 2'-OH group within the molecule for activity. The nucleic acids are
 CC useful for treating hepatitis B virus infection, hepatitis,
 CC hepatocellular carcinoma, cirrhosis and liver failure, either alone or in
 CC combination with other therapies such as lamivudine and interferons. The
 CC nucleic acids are useful as diagnostic tools to examine genetic drift and
 CC mutations within diseased cells, for detecting the presence of HBV RNA in
 CC a cell, for the study of RNA and for down-regulating gene expression of
 CC target genes in bacterial, fungal, viral, plant or mammalian cells. This
 CC sequence represents an enzymatic nucleic acid molecule which cleaves HBV
 CC RNA of the invention. Note: The sequence data for this patent is also
 CC available in electronic format from USPTO at
 CC seqdata.uspto.gov/sequence.html.
 CC
 SQ Sequence 38 BP; 11 A; 9 C; 10 G; 0 T; 7 U; 1 Other;
 Query Match 82.6%; Score 31.4; DB 12; Length 38;
 Best Local Similarity 94.1%; Pred. No. 0.00063;
 Matches 32; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 CCUGCAUUCGAGUAGGCCGUGAGCCGAAAAAU 34
 DB 1 CCUGCAUUCGAGUAGGCCGUGAGCCGAAAAAU 34

RESULT 10
 ACN26747
 ID ACN26747 standard; RNA; 38 BP.
 AC ACN26747;
 XX
 DT 22-APR-2004 (first entry)
 DE WNV minus strand Hammerhead Ribozyme SEQ ID NO 26763.
 XX
 KW WNV, West Nile Virus; antiinflammatory; cytoskeletal; hepatotropic;
 KW vironcide; neuroprotective; antibacterial; replication; pancreatitis;
 KW encephalitis; myocarditis; meningitis; infection; hepatitis;
 KW liver failure; cancer; cirrhosis; Hammerhead; inozyme; DNzyme;
 KW Amberzyme; Zinzyme; ss.
 XX
 OS West Nile Virus.
 XX
 PN WO200268637-A2.
 XX
 PD 06-SEP-2002.
 XX
 PF 19-OCT-2001; 2001WO-US048350.
 XX
 PR 20-OCT-2000; 2000US-0242411P.
 XX
 PA (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J A.
 XX
 PI Blatt L, Mcswiggen JA;

XX WPI; 2002-706994/76.
XX
XX New nucleic acid molecule that modulates replication of West Nile Virus
XX (WNV), useful for treating a condition related to WNV infection e.g.
XX pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX
XX Claim 24; SEQ ID NO 26763; 495bp; English.
XX
XX The invention relates to nucleic acid molecules that modulate replication
XX of the West Nile Virus (WNV). The nucleic acid molecules are useful for
XX treating a condition related to WNV infection e.g. pancreatitis,
XX encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
XX liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
XX molecule is selected from the group of ribozymes consisting of
XX Hammerhead, Inozyme, G-cleaver, DNazyme, Ambertzyme and Zinzyme. The
XX nucleic acid molecules further comprise at least five ribose residues, at
XX least ten 2'-O-methyl modifications, phosphorothioate linkages on at
XX least three of the 5' terminal nucleotides and a 3' end modification of a
XX 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
XX are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
XX in the specification. The present sequence is that of a nucleic acid
XX molecule of the invention
XX
XX Sequence 38 BP; 9 A; 10 C; 12 G; 0 T; 7 U; 0 Other;
XX
XX Query Match 82.1%; Score 31.2; DB 6; Length 38;
XX Best Local Similarity 91.7%; Pred. No. 0.00078;
XX Matches 33; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX
XX 2 CUGCAUUCUGAUGAGCGCCGUAAGCCGAAAUUACAG 37
XX 2 CUGCAGUCUGAUGAGCGCCGUAAGCCGAAAUACAG 37
XX
XX
XX RESULT 11
XX ACN27300
XX ID ACN27300 standard; RNA; 38 BP.
XX AC
XX ACN27300;
XX
XX 22-APR-2004 (first entry)
XX
XX WNV minus strand Hammerhead Ribozyme SEQ ID NO 27316.
XX
XX WNV, West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
XX virocidic; neuroprotective; antibacterial; replication; pancreatitis;
XX encephalitis; myocarditis; meningitis; infection; hepatitis;
XX liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
XX Ambertzyme; Zinzyme; ss.
XX
XX West Nile Virus.
XX
XX WO200268637-A2.
XX
XX 06-SEP-2002.
XX
XX 19-OCT-2001; 2001WO-US048350.
XX
XX 20-OCT-2000; 2000US-0242411P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX (BLAT/) BLATT L.
XX (MCSW/) MCSWIGEN J A.
XX
XX Blatt L, Mcswigen JA;
XX
XX WPI; 2002-706994/76.
XX
XX New nucleic acid molecule that modulates replication of West Nile Virus
XX (WNV), useful for treating a condition related to WNV infection e.g.
XX pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.

PS Claim 24; SEQ ID NO 27316; 495bp; English.
XX
XX The invention relates to nucleic acid molecules that modulate replication
XX of the West Nile Virus (WNV). The nucleic acid molecules are useful for
XX treating a condition related to WNV infection e.g. pancreatitis,
XX encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
XX liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
XX molecule is selected from the group of ribozymes consisting of
XX Hammerhead, Inozyme, G-cleaver, DNazyme, Ambertzyme and Zinzyme. The
XX nucleic acid molecules further comprise at least five ribose residues, at
XX least ten 2'-O-methyl modifications, phosphorothioate linkages on at
XX least three of the 5' terminal nucleotides and a 3' end modification of a
XX 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
XX are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
XX in the specification. The present sequence is that of a nucleic acid
XX molecule of the invention
XX
XX Sequence 38 BP; 11 A; 6 C; 13 G; 0 T; 8 U; 0 Other;
XX
XX Query Match 82.1%; Score 31.2; DB 6; Length 38;
XX Best Local Similarity 91.7%; Pred. No. 0.00078;
XX Matches 33; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX
XX 3 UGCAUUCUGAUGAGCGCCGUAAGCCGAAAUUACAG 38
XX 3 UGCAUUCUGAUGAGCGCCGUAAGCCGAAAUACAG 38
XX
XX
XX RESULT 12
XX ACN26250
XX ID ACN26250 standard; RNA; 38 BP.
XX AC
XX ACN26250;
XX
XX 22-APR-2004 (first entry)
XX
XX WNV minus strand Hammerhead Ribozyme SEQ ID NO 26266.
XX
XX WNV, West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
XX virocidic; neuroprotective; antibacterial; replication; pancreatitis;
XX encephalitis; myocarditis; meningitis; infection; hepatitis;
XX liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
XX Ambertzyme; Zinzyme; ss.
XX
XX West Nile Virus.
XX
XX WO200268637-A2.
XX
XX 06-SEP-2002.
XX
XX 19-OCT-2001; 2001WO-US048350.
XX
XX 20-OCT-2000; 2000US-0242411P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX (BLAT/) BLATT L.
XX (MCSW/) MCSWIGEN J A.
XX
XX Blatt L, Mcswigen JA;
XX
XX WPI; 2002-706994/76.
XX
XX New nucleic acid molecule that modulates replication of West Nile Virus
XX (WNV), useful for treating a condition related to WNV infection e.g.
XX pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX
XX Claim 24; SEQ ID NO 26266; 495bp; English.
XX
XX The invention relates to nucleic acid molecules that modulate replication
XX of the West Nile Virus (WNV). The nucleic acid molecules are useful for
XX treating a condition related to WNV infection e.g. pancreatitis,
XX encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
XX liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid

CC molecule is selected from the group of ribozymes consisting of
CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The
CC nucleic acid molecules further comprise at least five ribose residues, at
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC least three of the 5' terminal nucleotides and a 3' end modification of a
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC in the specification. The present sequence is that of a nucleic acid
CC molecule of the invention

CC
XX
SQ Sequence 38 BP; 13 A; 9 C; 10 G; 0 T; 6 U; 0 Other;

Query Match 81.1%; Score 30.8; DB 6; Length 38;
Best Local Similarity 94.1%; Pred. No. 0.0012;
Matches 32; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 5 CAUCUGAUGAGCGCCGUAAGCCGAAAAUUCAG 38
DB 5 CAGUCUGAUGAGCGCCGUAAGCCGAAAAUUCAG 38

RESULT 13
ACN26622
ID ACN26622 standard; RNA; 38 BP.
XX
AC ACN26622;
XX
XX 22-APR-2004 (first entry)
XX
XX
XX MNV minus strand Hammerhead Ribozyme SEQ ID NO 26638.
XX
XX MNV, West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
XX virucide; neuroprotective; antibacterial; replication; pancreatitis;
XX encephalitis; myocarditis; meningitis; infection; hepatitis;
XX liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
XX Amberzyme; Zinzyme; ss.
XX
XX West Nile Virus.
XX
XX WO200268637-A2.
XX
XX 06-SEP-2002.
XX
XX 19-OCT-2001; 2001WO-US048350.
XX
XX 20-OCT-2000; 2000US-0242411P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX (BLAT/) BLATT L.
XX (MCSW/) MCSWIGEN J A.
XX
XX Blatt L, Mcswigen JA;
XX
XX MPI, 2002-706994/76.
XX
XX New nucleic acid molecule that modulates replication of West Nile Virus
XX (MNV), useful for treating a condition related to MNV infection e.g.
XX pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX
XX Claim 24; SEQ ID NO 26638; 495bp; English.

CC The invention relates to nucleic acid molecules that modulate replication
CC of the West Nile Virus (MNV). The nucleic acid molecules are useful for
CC treating a condition related to MNV infection e.g. pancreatitis,
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
CC molecule is selected from the group of ribozymes consisting of
CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The
CC nucleic acid molecules further comprise at least five ribose residues, at
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC least three of the 5' terminal nucleotides and a 3' end modification of a
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC in the specification. The present sequence is that of a nucleic acid
CC molecule of the invention

CC in the specification. The present sequence is that of a nucleic acid
CC molecule of the invention

CC
XX
SQ Sequence 38 BP; 12 A; 7 C; 14 G; 0 T; 5 U; 0 Other;

Query Match 80.5%; Score 30.6; DB 6; Length 38;
Best Local Similarity 89.2%; Pred. No. 0.0014;
Matches 33; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 2 CUGCAUCUGAUGAGCGCCGUAAGCCGAAAAUUCAG 38
DB 2 CUGCAGACUGAUGAGCGCCGUAAGCCGAAAAUUCAG 38

RESULT 14
ACN27117
ID ACN27117 standard; RNA; 38 BP.
XX
AC ACN27117;
XX
XX 22-APR-2004 (first entry)
XX
XX
XX MNV minus strand Hammerhead Ribozyme SEQ ID NO 27133.
XX
XX MNV, West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
XX virucide; neuroprotective; antibacterial; replication; pancreatitis;
XX encephalitis; myocarditis; meningitis; infection; hepatitis;
XX liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNazyme;
XX Amberzyme; Zinzyme; ss.
XX
XX West Nile Virus.
XX
XX WO200268637-A2.
XX
XX 06-SEP-2002.
XX
XX 19-OCT-2001; 2001WO-US048350.
XX
XX 20-OCT-2000; 2000US-0242411P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX (BLAT/) BLATT L.
XX (MCSW/) MCSWIGEN J A.
XX
XX Blatt L, Mcswigen JA;
XX
XX MPI, 2002-706994/76.
XX
XX New nucleic acid molecule that modulates replication of West Nile Virus
XX (MNV), useful for treating a condition related to MNV infection e.g.
XX pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX
XX Claim 24; SEQ ID NO 27133; 495bp; English.

CC The invention relates to nucleic acid molecules that modulate replication
CC of the West Nile Virus (MNV). The nucleic acid molecules are useful for
CC treating a condition related to MNV infection e.g. pancreatitis,
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
CC molecule is selected from the group of ribozymes consisting of
CC Hammerhead, Inozyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The
CC nucleic acid molecules further comprise at least five ribose residues, at
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC least three of the 5' terminal nucleotides and a 3' end modification of a
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC in the specification. The present sequence is that of a nucleic acid
CC molecule of the invention

CC
XX
SQ Sequence 38 BP; 13 A; 7 C; 13 G; 0 T; 5 U; 0 Other;

Query Match 80.5%; Score 30.6; DB 6; Length 38;
Best Local Similarity 89.2%; Pred. No. 0.0014;

CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
 CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
 CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
 CC immune thrombocytopenia, and inflammatory arthropathy. The NOGO-
 CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the
 CC presence of a divalent cation that is preferably Mg^{2+} . Furthermore, the
 CC nucleic acid may be contacted with a cell to reduce NOGO activity of the
 CC cell and treat a patient having a condition associated with the level of
 CC NOGO. The treatment may further comprise the use of one or more
 CC therapies. In particular, the NOGO-targeting nucleic acid may be used to
 CC treat central nervous system (CNS) injury and cerebrovascular accident
 CC (CVA, stroke). Alzheimer's disease, dementia, multiple sclerosis (MS),
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
 CC disease, muscular dystrophy, and/or other neurodegenerative disease
 CC states which respond to the modulation of NOGO expression. The present
 CC sequence is a substrate sequence for a nucleic acid of the invention
 CC based on the human CD20 sequence

XX Sequence 38 BP; 10 A; 8 C; 10 G; 0 T; 10 U; 0 Other;

Query Match 80.0%; Score 30.4; DB 4; Length 38;

Best Local Similarity 96.9%; Pred. No. 0.0018; Mismatches 1; Indels 0; Gaps 0;

Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

5 CAUUCGAGGAGCGCGGUAAGCCGAAAUCA 36
 5 CAUUCGAGGAGCGCGGUAAGCCGAAAUCA 36

RESULT 17

ID ABRK05084 standard; RNA; 38 BP.

AC ABRK05084;

DT 12-MAR-2002 (first entry)

DE Human NOGO Inozyme substrate sequence #561.

XX Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
 XX cerebroprotective; neuroprotective; antiparkinsonian;
 XX muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
 XX DNazyme; inozyme; G-cleaver; amberyzyme; zinzyme; lymphoma; leukaemia;
 XX B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
 XX human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
 XX MCL; immunocytoma; IMC; immune thrombocytopenia; stroke; dementia;
 XX inflammatory arthropathy; central nervous system injury;
 XX cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
 XX chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
 XX Parkinson's disease; ataxia; Huntington's disease; substrate sequence;
 XX Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.

OS Homo sapiens.

OS Synthetic.

PN WO200159103-A2.

PD 16-AUG-2001.

PP 09-FEB-2001; 2001WO-US004273.

PR 11-FEB-2000; 2000US-0181797P.

PR 28-FEB-2000; 2000US-018516P.

PR 06-MAR-2000; 2000US-0187128P.

PA (RIBO-) RIBOZYME PHARM INC.

PA (BLAT/) BLATT L.

PA (MCSW/) MCSWIGGEN J.

PA (CHOW/) CHOWIRRA B M.

PI Blatt L, McSwiggen J, Chowirra BM;

DR WPI; 2001-607195/69.

XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
 PT constructs, which down regulate expression of a CD20 gene or neurite
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
 PT central nervous system injury.

PS Claim 89; Page 86; 200pp; English.

XX The invention relates to a nucleic acid molecule which down regulates
 CC expression of a CD20 gene and a nucleic acid molecule which down
 CC regulates expression of a neurite growth inhibitor gene (NOGO). The
 CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
 CC DNazyme) an inozyme (an endolytic nucleic acid cleaving an RNA molecule
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NNN motif)
 CC an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA
 CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA
 CC of CD20 in the presence of a divalent cation that is preferably Mg^{2+} .
 CC Furthermore, it may be contacted with a cell to reduce CD20 activity of
 CC the cell and treat a patient having a condition associated with the level
 CC of CD20. The treatment may further comprise the use of one or more
 CC therapies. In particular, the CD20 targeting nucleic acid may be used to
 CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
 CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
 CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
 CC immune thrombocytopenia, and inflammatory arthropathy. The NOGO-
 CC targeting nucleic acid is used to cleave RNA of the NOGO gene in the
 CC presence of a divalent cation that is preferably Mg^{2+} . Furthermore, the
 CC nucleic acid may be contacted with a cell to reduce NOGO activity of the
 CC cell and treat a patient having a condition associated with the level of
 CC NOGO. The treatment may further comprise the use of one or more
 CC therapies. In particular, the NOGO-targeting nucleic acid may be used to
 CC treat central nervous system (CNS) injury and cerebrovascular accident
 CC (CVA, stroke). Alzheimer's disease, dementia, multiple sclerosis (MS),
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
 CC disease, muscular dystrophy, and/or other neurodegenerative disease
 CC states which respond to the modulation of NOGO expression. The present
 CC sequence is a substrate sequence for a nucleic acid of the invention
 CC based on the human NOGO sequence

XX Sequence 38 BP; 10 A; 8 C; 9 G; 0 T; 10 U; 1 Other;

Query Match 80.0%; Score 30.4; DB 4; Length 38;

Best Local Similarity 93.9%; Pred. No. 0.0018; Mismatches 2; Indels 0; Gaps 0;

Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

2 CUGCAUUCGAGGAGCGCGGUAAGCCGAAAU 34
 2 CUGCAUUCGAGGAGCGCGGUAAGCCGAAAU 34

RESULT 18

ID ABRK04387 standard; RNA; 38 BP.

AC ABRK04387;

DT 12-MAR-2002 (first entry)

DE Human NOGO Hammerhead ribozyme substrate sequence #594.

XX Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
 XX cerebroprotective; neuroprotective; antiparkinsonian;
 XX muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
 XX DNazyme; inozyme; G-cleaver; amberyzyme; zinzyme; lymphoma; leukaemia;
 XX B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
 XX human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
 XX MCL; immunocytoma; IMC; immune thrombocytopenia; stroke; dementia;
 XX inflammatory arthropathy; central nervous system injury;
 XX cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
 XX chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;

KW Parkinson's disease; ataxia; Huntington's disease; substrate sequence;
KM Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
OS Homo sapiens.
XX Synthetic.
XX WO200159103-A2.
XX
XX 16-AUG-2001.
XX
XX 09-FEB-2001; 2001WO-US004273.
XX
XX 11-FEB-2000; 2000US-0181797P.
PR 28-FEB-2000; 2000US-0185516P.
PR 06-MAR-2000; 2000US-0187128P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA (BLATT/) BLATT L.
PA (MCSW/) MCSWIGEN J. A.
PA (CHOW/) CHOWRIRA B M.
XX
XX Blatt L, Mcswigen J, Chowrira BM;
PI WPI; 2001-607195/69.
XX
XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
PT constructs, which down regulate expression of a CD20 gene or neurite
PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
PT central nervous system injury.
XX
XX Claim 89; Page 75; 200P; English.
XX
XX The invention relates to a nucleic acid molecule which down regulates
CC expression of a CD20 gene and a nucleic acid molecule which down
CC regulates expression of a neurite growth inhibitor gene (NOCO). The
CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
CC DNAzyme) an Inozyme (an endolytic nucleic acid cleaving a an RNA molecule
CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) or
CC an amberzyme (cleaving RNA with an NGN triplet), a zinczyme (cleaving RNA
CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA
CC of CD20 in the presence of a divalent cation that is preferably Mg²⁺.
CC Furthermore, it may be contacted with a cell to reduce CD20 activity of
CC the cell and treat a patient having a condition associated with the level
CC of CD20. The treatment may further comprise the use of one or more
CC therapies. In particular, the CD20 targeting nucleic acid may be used to
CC treat lymphoma, leukemia, B-cell lymphoma, low-grade or follicular non-
CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
CC leukemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
CC immune thrombocytopenia, and inflammatory arthropathy. The NOCO-
CC targeting nucleic acid is used to cleave RNA of the NOCO gene in the
CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the
CC nucleic acid may be contacted with a cell to reduce NOCO activity of the
CC cell and treat a patient having a condition associated with the level of
CC NOCO. The treatment may further comprise the use of one or more
CC therapies. In particular, the NOCO-targeting nucleic acid may be used to
CC treat central nervous system (CNS) injury and cerebrovascular accident
CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
CC disease, muscular dystrophy, and/or other neurodegenerative disease
CC states which respond to the modulation of NOCO expression. The present
CC sequence is a substrate sequence for a nucleic acid of the invention
CC based on the human NOCO sequence
XX
XX Sequence 38 BP; 13 A; 9 C; 9 G; 0 T; 7 U; 0 Other;
SQ
Query Match 80.0%; Score 30.4; DB 4; Length 38;
Best Local Similarity 96.9%; Pred. No. 0.0018;
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

IDB 5 CAACCUUGAGAGCCGUUAGCCGAAAUCA 36
RESULT 19
ACN29362
ID ACN29362 standard; RNA; 38 BP.
XX
XX ACN29362;
XX
XX 22-APR-2004 (first entry)
XX
XX WNV minus strand Inozyme SEQ ID NO 29378.
DE
XX WNV; West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
KM virucide; neuroprotective; antibacterial; replication; pancreatitis;
KM encephalitis; myocarditis; meningitis; infection; hepatitis;
KM liver failure; cancer; cirrhosis; Hammanhead; Inozyme; DNAzyme;
KM Amberzyme; Zinczyme; ss.
XX
XX West Nile Virus.
OS
XX WO200268637-A2.
XX
XX 06-SEP-2002.
XX
XX 19-OCT-2001; 2001WO-US048350.
PF
XX 20-OCT-2000; 2000US-0242411P.
PR
XX (RIBO-) RIBOZYME PHARM INC.
PA (BLATT/) BLATT L.
PA (MCSW/) MCSWIGEN J A.
XX
XX Blatt L, Mcswigen JA;
PI WPI; 2002-706994/76.
XX
XX New nucleic acid molecule that modulates replication of West Nile Virus
PT (WNV), useful for treating a condition related to WNV infection e.g.
PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX
XX Claim 24; SEQ ID NO 29378; 495P; English.
XX
XX The invention relates to nucleic acid molecules that modulate replication
CC of the West Nile Virus (WNV). The nucleic acid molecules are useful for
CC treating a condition related to WNV infection e.g. pancreatitis,
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
CC molecule is selected from the group of ribozymes consisting of
CC Hammanhead, Inozyme, G-cleaver, DNAzyme, Amberzyme and zinczyme. The
CC nucleic acid molecules further comprise at least five ribose residues, at
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC least three of the 5' terminal nucleotides and a 3' end modification of a
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC in the specification. The present sequence is that of a nucleic acid
XX molecule of the invention
XX
XX Sequence 38 BP; 11 A; 7 C; 11 G; 0 T; 8 U; 1 Other;
SQ
Query Match 80.0%; Score 30.4; DB 6; Length 38;
Best Local Similarity 93.9%; Pred. No. 0.0018;
Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

XX Sequence 38 BP; 11 A; 6 C; 14 G; 0 T; 7 U; 0 Other;
SQ

Query Match 79.5%; Score 30.2; DB 6; Length 38;
Best Local Similarity 91.4%; Pred. No. 0.0022;
Matches 32; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 GCAUUCUGAUGAGCGCGUUGAGCGCGAUAUUCAG 38
DB 4 GCAUUCUGAUGAGCGCGUUGAGCGCGAUAUUCAG 38

RESULT 22

ACN30394
ID ACN30394 standard; RNA; 38 BP.

XX ACN30394;

XX 22-APR-2004 (first entry)

DE WNV minus strand Inozyme SEQ ID NO 30410.

XX WNV, West Nile Virus; antiinflammatory; cytostatic; hepatotropic;
XX virucide; neuroprotective; antibacterial; replication; pancreatitis;
XX encephalitis; myocarditis; meningitis; infection; hepatitis;
XX liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;
XX Amberzyme; Zinzyme; ss.

OS West Nile Virus.

XX WO200268637-A2.

XX 06-SEP-2002.

XX 19-OCT-2001; 2001WO-US048350.

XX 20-OCT-2000; 2000US-0242411P.

XX (RIBO-) RIBOZYME PHARM INC.

XX (BLAT/) BLATT L.

XX (MCSW/) MCSWIGEN J A.

XX Blatt L, Mcswiggen JA;

XX WPI: 2002-706994/76.

XX New nucleic acid molecule that modulates replication of West Nile Virus
(WNV), useful for treating a condition related to WNV infection e.g.
pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.

XX Claim 24; SEQ ID NO 30410; 495pp; English.

XX The invention relates to nucleic acid molecules that modulate replication
of the West Nile Virus (WNV). The nucleic acid molecules are useful for
treating a condition related to WNV infection e.g. pancreatitis,
encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
molecule is selected from the group of ribozymes consisting of
Hammerhead, Inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyme. The
nucleic acid molecules further comprise at least five ribose residues, at
least ten 2'-O-methyl modifications, phosphorothioate linkages on at
least three of the 5' terminal nucleotides and a 3' end modification of a
3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
in the specification. The present sequence is that of a nucleic acid
molecule of the invention

XX Sequence 38 BP; 9 A; 9 C; 11 G; 0 T; 8 U; 1 Other;

Query Match 79.5%; Score 30.2; DB 6; Length 38;
Best Local Similarity 88.9%; Pred. No. 0.0022;
Matches 32; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 CUGCAUUCUGAUGAGCGCGUUGAGCGCGAUAUUCAG 37
DB 2 CUGCCUUCUGAUGAGCGCGUUGAGCGCGAUAUUCAG 37

RESULT 23

AAH96054
ID AAH96054 standard; RNA; 38 BP.

XX AAH96054;

XX 09-OCT-2001 (first entry)

DE Human Chk1 ribozyme SEQ ID NO: 1479.

XX Human; checkpoint kinase-1; Chk1; antisense; ribozyme; gene therapy;

XX RNA cleavage; cancer; ss.

XX Homo sapiens.

XX WO200157206-A2.

XX 09-AUG-2001.

XX 02-FEB-2001; 2001WO-US003504.

XX 03-FEB-2000; 2000US-0179983P.

XX (RIBO-) RIBOZYME PHARM INC.

XX (FATT/) FATTAEY A R.

XX Fatcaey AR, Jarvis T, Mcswiggen J, Booher RN, Holman PS;

XX WPI: 2001-496922/54.

XX Novel nucleic acid molecule e.g., ribozymes or antisense nucleic acid
molecules, which downregulates expression of a checkpoint kinase-1 gene,
useful for treating colorectal, lung, breast or prostate cancers.

XX Claim 5; Page 53; 115pp; English.

XX The present invention provides nucleic acid molecules capable of
downregulating the expression of the human checkpoint kinase-1 (Chk1)
gene. These may be antisense or ribozyme sequences, and are useful in the
treatment of diseases associated with conditions affected by Chk1 levels,
including cancer. The present sequence is an oligonucleotide described in
the exemplification of the invention

XX Sequence 38 BP; 8 A; 9 C; 12 G; 0 T; 9 U; 0 Other;

Query Match 78.9%; Score 30; DB 4; Length 38;
Best Local Similarity 86.8%; Pred. No. 0.0026;
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CCUGCAUUCUGAUGAGCGCGUUGAGCGCGAUAUUCAG 38
DB 1 CCUGCAUUCUGAUGAGCGCGUUGAGCGCGAUAUUCAG 38

RESULT 24

ABKS8289
ID ABKS8289 standard; RNA; 38 BP.

XX ABKS8289;

XX 02-JUL-2002 (first entry)

DE Human CLCA1 gene enzymatic nucleic acid #2660.

XX Human; chloride channel activated 1; CLCA1; ss; antiasthmatic;
XX antiinflammatory; chronic obstructive pulmonary disease; COPD; asthma;
XX chronic bronchitis; cystic fibrosis; obstructive bowel syndrome;
XX oxygen therapy; bronchodilator; corticosteroid; vaccination; mucokinetic;

XX acetylcysteine.
XX Homo sapiens.
XX WO200211674-A2.
XX 14-FEB-2002.
XX 09-AUG-2001; 2001WO-US024970.
XX 09-AUG-2000; 2000US-0224383P.
XX (RIBO-) RIBOZYME PHARM INC.
XX (SINT) SINTEX USA LLC.
XX (THOM/) THOMPSON J.
XX Thompson J, Mcswiggen J, McKenzie T, Ayers D, Szymkowski DE;
XX Grupe A;
XX WPI; 2002-217145/27.
XX Enzymatic polynucleotide that down regulates expression of chloride
XX channel calcium activated gene, useful for treating Chronic obstructive
XX pulmonary disease (COPD), chronic bronchitis and asthma.
XX Claim 5; Page 61; 152pp; English.
XX The invention relates to enzymatic nucleic acid molecules that down
XX regulate expression of chloride channel calcium activated 1 (ClCA1) genes
XX by cleaving RNA derived from the genes. The nucleic acid sequences are
XX useful as pharmaceutical agents for treating conditions such as chronic
XX obstructive pulmonary disease (COPD), chronic bronchitis, asthma, cystic
XX fibrosis, obstructive bowel syndrome and any other diseases or conditions
XX that are related to or will respond to the levels of ClCA1 in a cell or
XX tissue. The sequences are useful for reducing ClCA1 activity in a cell,
XX hence, are useful for treatment of a patient having a condition
XX associated with the level of ClCA1, where the invention further comprises
XX the use of one or more therapies under conditions suitable for the
XX treatment, for example, oxygen therapy, bronchodilators, corticosteroids,
XX antibacterials, vaccinations, acetylcysteine and mucokinetic agents. The
XX nucleic acids of the invention are also used as diagnostic tools to
XX examine genetic drift and mutations within diseased cells or to detect
XX the presence of ClCA1 RNA in a cell. This sequence represents an
XX enzymatic nucleic acid molecule of the invention
XX
XX Sequence 38 BP; 14 A; 7 C; 10 G; 0 T; 7 U; 0 Other;
SQ
Query Match 78.9%; Score 30; DB 6; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0026;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 GCAAUUCUGAUGAGCCGUTUAGCCGAAAAA 33
DB 4 GCAAUUCUGAUGAGCCGUTUAGCCGAAAAA 33
RESULT 25
ID ACN26440 standard; RNA; 38 BP.
XX ACN26440;
XX ACN26440;
XX 22-APR-2004 (first entry)
XX
XX MNV minus strand Hammerhead Ribozyme SEQ ID NO 26456.
XX
XX MNV; West Nile Virus; antiinflammatory; cyrostatic; hepatotropic;
XX viruside; neuroprotective; antibacterial; replication; pancreatitis;
XX encephalitis; myocardiatis; meningitis; infection; hepatitis;
XX liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;
XX Amberzyme; Zinzyne; ss.
XX
XX West Nile Virus.
XX

XX WO200268637-A2.
XX 06-SEP-2002.
XX 19-OCT-2001; 2001WO-US048350.
XX 20-OCT-2000; 2000US-0242411P.
XX (RIBO-) RIBOZYME PHARM INC.
XX (BLAT/) BLATT L.
XX (MCSW/) MCSWIGGEN J A.
XX Blact L, Mcswiggen JA;
XX WPI; 2002-706994/76.
XX New nucleic acid molecule that modulates replication of West Nile Virus
XX (MNV), useful for treating a condition related to MNV infection e.g.
XX pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
XX Claim 24; SEQ ID NO 26456; 495pp; English.
XX The invention relates to nucleic acid molecules that modulate replication
XX of the West Nile Virus (MNV). The nucleic acid molecules are useful for
XX treating a condition related to MNV infection e.g. pancreatitis,
XX encephalitis, myocardiatis, meningitis, neurologic infection, hepatitis,
XX liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
XX molecule is selected from the group of ribozymes consisting of
XX Hammerhead, Inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyne. The
XX nucleic acid molecules further comprise at least five ribose residues, at
XX least ten 2'-O-methyl modifications, phosphorothioate linkages on at
XX least three of the 5' terminal nucleotides and a 3' end modification of a
XX 3',3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
XX are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
XX in the specification. The present sequence is that of a nucleic acid
XX molecule of the invention
XX
XX Sequence 38 BP; 12 A; 8 C; 13 G; 0 T; 5 U; 0 Other;
SQ
Query Match 78.9%; Score 30; DB 6; Length 38;
Best Local Similarity 86.8%; Pred. No. 0.0026;
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 CCUGCAUUCUGAUGAGCCGUTUAGCCGAAAAAUCAGG 38
DB 1 CCAGACUCUGAUGAGCCGUTUAGCCGAAAAAAGAGG 38
RESULT 26
ID ACN26144 standard; RNA; 38 BP.
XX ACN26144;
XX ACN26144;
XX 22-APR-2004 (first entry)
XX
XX MNV minus strand Hammerhead Ribozyme SEQ ID NO 26160.
XX
XX MNV; West Nile Virus; antiinflammatory; cyrostatic; hepatotropic;
XX viruside; neuroprotective; antibacterial; replication; pancreatitis;
XX encephalitis; myocardiatis; meningitis; infection; hepatitis;
XX liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;
XX Amberzyme; Zinzyne; ss.
XX
XX West Nile Virus.
XX
XX WO200268637-A2.
XX 06-SEP-2002.
XX 19-OCT-2001; 2001WO-US048350.
XX

PR 20-OCT-2000; 2000US-0242411P.
XX (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MCSM/) MCSWIGEN J A.
XX
XX Blatt L, Mcswiggen JA;
XX WPI; 2002-706994/76.
DR
XX
XX New nucleic acid molecule that modulates replication of West Nile Virus
PT (MNV), useful for treating a condition related to MNV infection e.g.
PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
PS
XX Claim 24; SEQ ID NO 26160; 495bp; English.
XX
XX The invention relates to nucleic acid molecules that modulate replication
CC of the West Nile Virus (MNV). The nucleic acid molecules are useful for
CC treating a condition related to MNV infection e.g. pancreatitis,
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
CC molecule is selected from the group of ribozymes consisting of
CC Hammerhead, Iboxyme, G-cleaver, DNazyme, Amberzyme and Zinzyme. The
CC nucleic acid molecules further comprise at least five ribose residues, at
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC least three of the 5' terminal nucleotides and a 3' end modification of a
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC in the specification. The present sequence is that of a nucleic acid
CC molecule of the invention
CC
SQ Sequence 38 BP; 10 A; 9 C; 10 G; 0 T; 9 U; 0 Other;
Query Match 78.9%; Score 30; DB 6; Length 38;
Best Local Similarity 86.8%; Pred. No. 0.0026; 5; Indels 0; Gaps 0;
Matches 33; Conservative 0; Mismatches 5;
QY 1 CCUGCAUUCUGAUGAGCCGCUUAGGCCGAAAUUACAGG 38
1 CUUGCAUUCUGAUGAGCCGCUUAGGCCGAAAUUACAGG 38
Db
RESULT 27
ACD50521
ID ACD50521 standard; RNA; 38 BP.
XX
AC ACD50521;
XX
DT 23-SEP-2003 (first entry)
XX
DE HBV hammerhead ribozyme sequence #89.
XX
XX Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
KW RNA stability; RNA expression; RNA synthesis; antisense;
KW enzymatic nucleic acid; hammerhead ribozyme; DNazyme; zinzyme;
KW amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;
KW HBV reverse transcriptase; Enhancer I region; viral replication;
KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;
KW liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
KW virucide; antiinflammatory; ss.
XX
XX Hepatitis B virus.
OS
XX
XX WO200281494-A1.
PN
XX
XX 17-OCT-2002.
PD
XX
XX 26-MAR-2002; 2002WO-US009187.
PF
XX
XX 26-MAR-2001; 2001US-00817879.
PR 08-JUN-2001; 2001US-00877478.
PR 08-JUN-2001; 2001US-0296876P.
PR 24-OCT-2001; 2001US-0335059P.

PR 05-DEC-2001; 2001US-0337055P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MACE/) MACEJAK D.
PA (MCSM/) MCSWIGEN J.
PA (MORR/) MORRISSEY D.
PA (PAVC/) PAVCO P.
PA (LEBP/) LEE P.
PA (DRAP/) DRAPER K.
PA (ROBE/) ROBERTS E.
XX
XX Blatt L, Macejak D, Mcswiggen J, Morrissey D, Pavco P, Lee P;
PI Draper K, Roberts E;
XX WPI; 2003-229207/22.
DR
XX
XX Novel compound useful for treating cirrhosis, liver failure,
PT hepatocellular carcinoma, or condition associated with hepatitis C virus
PT infection.
PT
XX
PS Example 1; Page 137; 387bp; English.
XX
XX The present invention relates to nucleic acid molecules which modulate
CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or
CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense
CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,
CC inozymes, zinzymes, amberzymes, and G-cleaver ribozymes. Also disclosed
CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse
CC transcriptase and/or HBV reverse transcriptase primer sequences, as well
CC as oligonucleotides that specifically bind the Enhancer I region of HBV
CC DNA. The nucleic acids may be used to modulate the expression of HBV
CC genes and HBV viral replication. Also disclosed is a method for screening
CC compounds and/or potential therapies directed against HBV, and compounds
CC that modulate the expression and/or replication of HCV. The compounds and
CC methods of the invention are useful for the treatment of degenerative and
CC disease states related to HBV and HCV infection, replication and gene
CC expression such as cirrhosis, liver failure, and hepatocellular
CC carcinoma. The present sequence represents one of the HBV ribozyme,
CC inozyme, G-cleaver, zinzyme, DNazyme or amberzyme sequences disclosed in
CC the present invention
CC
SQ Sequence 38 BP; 12 A; 8 C; 13 G; 0 T; 5 U; 0 Other;
Query Match 78.9%; Score 30; DB 8; Length 38;
Best Local Similarity 86.8%; Pred. No. 0.0026; 5; Indels 0; Gaps 0;
Matches 33; Conservative 0; Mismatches 5;
QY 1 CCUGCAUUCUGAUGAGCCGCUUAGGCCGAAAUUACAGG 38
1 CCAACAAGCTUGAUGAGCCGCUUAGGCCGAAAGUAGG 38
Db
RESULT 28
ADL53551
ID ADL53551 standard; RNA; 38 BP.
XX
AC ADL53551;
XX
DT 20-MAY-2004 (first entry)
XX
XX Human IKK-gamma ribozyme sequence #29.
DE
XX
XX antisense oligonucleotide; neurite growth inhibitor; NOGO;
KW prostaglandin D2 receptor; PTGDR; Ikappab kinase; IKK;
KW protein kinase PKR; cerebrovascular accident;
KW central nervous system injury; CNS injury; spinal cord injury; cancer;
KW melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;
KW restenosis; asthma; Crohn's disease; diabetes; obesity;
KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;
KW graft rejection; ischemia; reperfusion; glomerulonephritis; sepsis;
KW allergy; asthma; allergic rhinitis; atopic dermatitis;
KW IKK-gamma ribozyme; substrate; ss; human.

XX OS Homo sapiens.
 XX PN WO200281628-A2.
 XX PD 17-OCT-2002.
 XX PF 03-APR-2002; 2002WO-US010512.
 XX PR 05-APR-2001; 2001US-00827395.
 XX PR 29-MAY-2001; 2001US-0294412P.
 XX PR 28-AUG-2001; 2001US-0315315P.
 XX PA (RIBO-) RIBOZYME PHARM INC.
 XX PI Blatt L, Chowrira B, Haeblerl P, Mcswiggen J, Fosnaugh K;
 XX DR WPI; 2003-058513/05.
 XX PT Novel enzymatic nucleic acid that down-regulates expression of neurite
 PT growth inhibitor receptor, prostaglandin D2 receptor, Ikappab kinase or
 PT protein kinase PKR genes, for treating cancer and inflammatory disease.
 XX PS Claim 57; SEQ ID NO 7084; 317pp; English.
 CC The invention comprises nucleic acids (e.g. antisense oligonucleotides)
 CC that down regulate the expression or inhibit the function of a receptor
 CC for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),
 CC Ikappab kinase (IKK), or protein kinase PKR. The nucleic acids of the
 CC invention are useful for treating: cerebrovascular accident, central
 CC nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,
 CC lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,
 CC restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune
 CC disease, lupus, multiple sclerosis, transplant/graft rejection,
 CC ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic
 CC conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The
 CC nucleic acids of the invention are also useful for down-regulating the
 CC expression of a target gene and as a diagnostic tool to examine genetic
 CC drifts and mutations within diseased cells or to detect the presence of a
 CC target RNA in a cell. The present RNA sequence represents a human IKK-
 CC gamma ribozyme sequence.
 CC
 SQ Sequence 38 BP; 8 A; 9 C; 13 G; 0 T; 8 U; 0 Other;
 Query Match 78.9%; Score 30; DB 11; Length 38;
 Best Local Similarity 86.8%; Pred. No. 0.0026;
 Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 CCUGCAUUCGUAUGAGCCGCUUAGGCCGAAAUUACAAG 38
 Db 1 CCUGUUCUCUGAUGAGCCGCUUAGGCCGAAAUUAGCAGG 38
 RESULT 29
 ADL55719
 ID ADL55719 standard; RNA; 38 BP.
 AC ADL55719;
 XX
 XX 20-MAY-2004 (first entry)
 XX
 DE Human PKR ribozyme sequence #183.
 XX
 DE antisense oligonucleotide; neurite growth inhibitor; NOGO;
 KW prostaglandin D2 receptor; PTGDR; Ikappab kinase; IKK;
 KW protein kinase PKR; cerebrovascular accident;
 KW central nervous system injury; CNS injury; spinal cord injury; cancer;
 KW melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;
 KW restenosis; asthma; Crohn's disease; diabetes; obesity;
 KW autoimmune disease; lupus; multiple sclerosis; transplant rejection;
 KW graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;
 KW allergy; asthma; allergic rhinitis; atopic dermatitis; PKR ribozyme;
 KW substrate; ss; human.

XX OS Homo sapiens.
 XX PN WO200281628-A2.
 XX PD 17-OCT-2002.
 XX PF 03-APR-2002; 2002WO-US010512.
 XX PR 05-APR-2001; 2001US-00827395.
 XX PR 29-MAY-2001; 2001US-0294412P.
 XX PR 28-AUG-2001; 2001US-0315315P.
 XX PA (RIBO-) RIBOZYME PHARM INC.
 XX PI Blatt L, Chowrira B, Haeblerl P, Mcswiggen J, Fosnaugh K;
 XX DR WPI; 2003-058513/05.
 XX PT Novel enzymatic nucleic acid that down-regulates expression of neurite
 PT growth inhibitor receptor, prostaglandin D2 receptor, Ikappab kinase or
 PT protein kinase PKR genes, for treating cancer and inflammatory disease.
 XX PS Claim 57; SEQ ID NO 9252; 317pp; English.
 CC The invention comprises nucleic acids (e.g. antisense oligonucleotides)
 CC that down regulate the expression or inhibit the function of a receptor
 CC for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),
 CC Ikappab kinase (IKK), or protein kinase PKR. The nucleic acids of the
 CC invention are useful for treating: cerebrovascular accident, central
 CC nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,
 CC lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,
 CC restenosis or asthma), Crohn's disease, diabetes, obesity, autoimmune
 CC disease, lupus, multiple sclerosis, transplant/graft rejection,
 CC ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic
 CC conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The
 CC nucleic acids of the invention are also useful for down-regulating the
 CC expression of a target gene and as a diagnostic tool to examine genetic
 CC drifts and mutations within diseased cells or to detect the presence of a
 CC target RNA in a cell. The present RNA sequence represents a human PKR
 CC ribozyme sequence.
 CC
 SQ Sequence 38 BP; 11 A; 7 C; 8 G; 0 T; 12 U; 0 Other;
 Query Match 78.9%; Score 30; DB 11; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0.0026;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 AAUCUGAUGAGGCCGCUUAGGCCGAAAUUAC 35
 Db 6 AAUCUGAUGAGGCCGCUUAGGCCGAAAUUAC 35
 RESULT 30
 ADM60497
 ID ADM60497 standard; RNA; 38 BP.
 AC ADM60497;
 XX
 XX 03-JUN-2004 (first entry)
 XX
 DE Hepatitis B virus (HBV) enzymatic nucleic acid #89.
 XX
 DE Hepatitis B virus (HBV); ss; enzymatic nucleic acid; RNA cleavage;
 KW hepatitis B virus infection; hepatitis; hepatocellular carcinoma;
 KW cirrhosis; liver failure; lamivudine; interferon; genetic drift;
 KW virucide; hepatotropic; antiinflammatory; cytostatic.
 XX
 OS Hepatitis B virus.
 XX US2004054156-A1.
 XX PN 18-MAR-2004.
 XX PD

PF	15-JAN-2003;	2003US-00342902.
XX		
XX	14-MAY-1992;	92US-00882712.
PR	07-FEB-1994;	94US-00193627.
PR	08-NOV-1999;	99US-00436430.
PR	20-MAR-2000;	2000US-00531025.
PR	09-AUG-2000;	2000US-00536385.
PR	24-OCT-2000;	2000US-00596347.
PR	08-JUN-2001;	2001US-00877478.
XX		
PA	(DRAP/) DRAPER K.	
PA	(BLAT/) BLATT L.	
PA	(MCSW/) MCSWIGGEN J A.	
XX	(MORR/) MORRISSEY D.	
PI	Draper K, Blatt L, Mcswiggen JA, Morrissey D;	
XX		
DR	WPI: 2004-247781/23.	
XX		
PT	Novel enzymatic nucleic acid molecule such as DNAsymes and inozymes	
PT	specifically cleaving RNA derived from hepatitis B virus and comprising	
PT	one or more binding arms, useful for treating hepatitis and cirrhosis.	
XX		
PS	Disclosure; SEQ ID NO 2631; 122pp; English.	
XX		
CC	The invention relates to an enzymatic nucleic acid molecule that	
CC	specifically cleaves RNA derived from hepatitis B virus (HBV) and	
CC	comprising one or more binding arms, without requiring the presence of a	
CC	2'-OH group within the molecule for activity. The nucleic acids are	
CC	useful for treating hepatitis B virus infection, hepatitis,	
CC	hepatocellular carcinoma, cirrhosis and liver failure, either alone or in	
CC	combination with other therapies such as lamivudine and interferons. The	
CC	nucleic acids are useful as diagnostic tools to examine genetic drift and	
CC	mutations within diseased cells, for detecting the presence of HBV RNA in	
CC	a cell, for the study of RNA and for down-regulating gene expression of	
CC	target genes in bacterial, fungal, viral, plant or mammalian cells. This	
CC	sequence represents an enzymatic nucleic acid molecule which cleaves HBV	
CC	RNA of the invention. Note: The sequence data for this patent is also	
CC	available in electronic format from USPTO at	
CC	seqdata.uspto.gov/sequence.html.	
XX		
SQ	Sequence 38 BP; 12 A; 8 C; 13 G; 0 T; 5 U; 0 Other;	
	Query Match	78.9%; Score 30; DB 12; Length 38;
	Best Local Similarity	86.8%; Pred. No. 0.0026;
	Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;	
QY	1 CCUGCAUUCUGAUGAGCGCGUUGAGCGCCGAAAUAUACAGG 38	
	1 CCAACAAACUGAUGAGCGCGUUGAGCGCCGAAAUAUACAGG 38	
DB		
RESULT 31		
ID	ABK07861	
XX	ABK07861 standard; RNA; 38 BP.	
XX		
XX	ABK07861;	
XX		
DT	12-MAR-2002 (first entry)	
DE		
XX	Human CD20 Hammerhead ribozyme substrate sequence #104.	
XX		
KW	Human; ss; antisense therapy; cytosstatic; antiinflammatory; haemostatic;	
KW	cerebroprotective; nootropic; neuroprotective; antiparkinsonian;	
KW	muscular; CD20; neurite growth inhibitor gene; NOCO; hammerhead ribozyme;	
KW	DNAzyme; inozyme; G-cleaver; ambezyme; zinzyme; lymphoma; leukaemia;	
KW	B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;	
KW	human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;	
KW	MCL; immunocytoma; IMC; immune thrombocytopenia; stroke; dementia;	
KW	inflammatory arthropathy; central nervous system injury;	
KW	cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;	
KW	chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;	

KW Parkinson's disease; ataxia; Huntington's disease; substrate sequence;
 KM Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
 OS Synthetic.
 XX
 XX MO200159103-A2.
 XX
 XX
 XX 16-AUG-2001.
 XX
 XX
 XX 09-FEB-2001; 2001WO-US004273.
 XX
 XX 11-FEB-2000; 2000US-0181797P.
 PR 28-FEB-2000; 2000US-0185516P.
 PR 06-MAR-2000; 2000US-0187128P.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGGEN J.
 PA (CHOW/) CHOWRIRA B M.
 XX
 PI Blatt L, Mcswiggen J, Chowrira BM;
 DR WPI; 2001-607195/69.
 XX
 XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
 PT constructs, which down regulate expression of a CD20 gene or neurite
 PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
 PT central nervous system injury.
 XX
 XX
 XX Claim 31; Page 141; 2000p; English.
 XX
 XX The invention relates to a nucleic acid molecule which down regulates
 CC expression of a CD20 gene and a nucleic acid molecule which down
 CC regulates expression of a neurite growth inhibitor gene (NOCO). The
 CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
 CC DNzyme) an inozyme (an endolytic nucleic acid cleaving an RNA molecule
 CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) or
 CC an amberzyme (cleaving RNA with an NGN triplet), a zinczyme (cleaving RNA
 CC with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA
 CC of CD20 in the presence of a divalent cation that is preferably Mg²⁺.
 CC Furthermore, it may be contacted with a cell to reduce CD20 activity of
 CC the cell and treat a patient having a condition associated with the level
 CC of CD20. The treatment may further comprise the use of one or more
 CC therapies. In particular, the CD20 targeting nucleic acid may be used to
 CC treat lymphoma, leukemia, B-cell lymphoma, low-grade or follicular non-
 CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
 CC leukemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
 CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
 CC immune thrombocytopenia, and inflammatory arthropathy. The NOCO-
 CC targeting nucleic acid is used to cleave RNA of the NOCO gene in the
 CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the
 CC nucleic acid may be contacted with a cell to reduce NOCO activity of the
 CC cell and treat a patient having a condition associated with the level of
 CC NOCO. The treatment may further comprise the use of one or more
 CC therapies. In particular, the NOCO-targeting nucleic acid may be used to
 CC treat central nervous system (CNS) injury and cerebrovascular accident
 CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
 CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
 CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
 CC disease, muscular dystrophy, and/or other neurodegenerative disease
 CC states which respond to the modulation of NOCO expression. The present
 CC sequence is a substrate sequence for a nucleic acid of the invention
 CC based on the human CD20 sequence
 XX
 XX Sequence 38 BP; 11 A; 8 C; 10 G; 0 T; 9 U; 0 Other;
 SQ
 XX
 XX Query Match 78.4%; Score 29.8; DB 4; Length 38;
 XX Best Local Similarity 93.9%; Pred. No. 0.0032;
 XX Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0.

DB 2 CUCUAUCUGAGGCCGUGGCCGAAAAAU 34

RESULT 32
ABK04290
ID ABK04290 standard; RNA; 38 BP.
XX
XX ABK04290;
XX
XX 12-MAR-2002 (first entry)
XX
XX Human NCOG Hammerhead ribozyme substrate sequence #497.
XX
XX Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
XX cerebrioprotective; neurotropic; neuroprotective; antiparkinsonian;
XX muscular; CD20; neurite growth inhibitor gene; NCOG; hammerhead ribozyme;
XX DNazyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia;
XX B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
XX human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
XX MCL; immunocytoma; IMC; immune thrombocytopenia; stroke; dementia;
XX inflammatory arthropathy; central nervous system injury;
XX cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
XX chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
XX Parkinson's disease; ataxia; Huntington's disease; substrate sequence;
XX Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX WO200159103-A2.
XX
XX 16-AUG-2001.
XX
XX 09-FEB-2001; 2001WO-US004273.
XX
XX 11-FEB-2000; 2000US-0181797P.
XX 28-FEB-2000; 2000US-0185516P.
XX 06-MAR-2000; 2000US-0187128P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX (BLAT/) BLATT L.
XX (MCSW/) MCSWIGGEN J.
XX (CHOW/) CHOWRIRA B M.
XX
XX Blatt L, Mcswiggen J, Chowrira BM;
XX
XX WPI; 2001-607195/69.
XX
XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
XX constructs, which down regulate expression of a CD20 gene or neurite
XX growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
XX central nervous system injury.
XX
XX Claim 89; Page 73; 200pp; English.
XX
XX The invention relates to a nucleic acid molecule which down regulates
XX expression of a CD20 gene and a nucleic acid molecule which down
XX regulates expression of a neurite growth inhibitor gene (NCOG). The
XX nucleic acids may be enzymatic nucleic acids (e.g., a ribozyme or a
XX DNazyme) an inozyme (an endolytic nucleic acid cleaving an RNA molecule
XX possessing an NCH motif), a G-cleaver (cleaving RNA with a NTN motif) or
XX an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA
XX with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA
XX of CD20 in the presence of a divalent cation that is preferably Mg²⁺.
XX Furthermore, it may be contacted with a cell to reduce CD20 activity of
XX the cell and treat a patient having a condition associated with the level
XX of CD20. The treatment may further comprise the use of one or more
XX therapies. In particular, the CD20 targeting nucleic acid may be used to
XX treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
XX Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
XX leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
XX lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
XX immune thrombocytopenia, and inflammatory arthropathy. The NCOG-

CC targeting nucleic acid is used to cleave RNA of the NCOG gene in the
CC presence of a divalent cation that is preferably Mg²⁺. Furthermore, the
CC nucleic acid may be contacted with a cell to reduce NCOG activity of the
CC cell and treat a patient having a condition associated with the level of
CC NCOG. The treatment may further comprise the use of one or more
CC therapies. In particular, the NCOG-targeting nucleic acid may be used to
CC treat central nervous system (CNS) injury and cerebrovascular accident
CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
CC disease, muscular dystrophy, and/or other neurodegenerative disease
CC states which respond to the modulation of NCOG expression. The present
CC sequence is a substrate sequence for a nucleic acid of the invention
CC based on the human NCOG sequence
CC
SQ Sequence 38 BP; 11 A; 9 C; 13 G; 0 T; 5 U; 0 Other;
Query Match 78.4%; Score 29.8; DB 4; Length 38;
Best Local Similarity 93.9%; Pred. No. 0.0032;
Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 4 GCAUUCUGAGGCCGUGGCCGAAAAAUCA 36
DB 4 GCAUUCUGAGGCCGUGGCCGAAAAAGCA 36
RESULT 33
ABK04122
ID ABK04122 standard; RNA; 38 BP.
XX
XX ABK04122;
XX
XX 12-MAR-2002 (first entry)
XX
XX Human NCOG Hammerhead ribozyme substrate sequence #329.
XX
XX Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
XX cerebrioprotective; neurotropic; neuroprotective; antiparkinsonian;
XX muscular; CD20; neurite growth inhibitor gene; NCOG; hammerhead ribozyme;
XX DNazyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia;
XX B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
XX human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
XX MCL; immunocytoma; IMC; immune thrombocytopenia; stroke; dementia;
XX inflammatory arthropathy; central nervous system injury;
XX cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
XX chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
XX Parkinson's disease; ataxia; Huntington's disease; substrate sequence;
XX Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
XX
XX Homo sapiens.
XX Synthetic.
XX
XX WO200159103-A2.
XX
XX 16-AUG-2001.
XX
XX 09-FEB-2001; 2001WO-US004273.
XX
XX 11-FEB-2000; 2000US-0181797P.
XX 28-FEB-2000; 2000US-0185516P.
XX 06-MAR-2000; 2000US-0187128P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX (BLAT/) BLATT L.
XX (MCSW/) MCSWIGGEN J.
XX (CHOW/) CHOWRIRA B M.
XX
XX Blatt L, Mcswiggen J, Chowrira BM;
XX
XX WPI; 2001-607195/69.
XX
XX Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
XX constructs, which down regulate expression of a CD20 gene or neurite

PT growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
PT central nervous system injury.

PS Claim 89; Page 71; 200pp; English.

The invention relates to a nucleic acid molecule which down regulates expression of a CD20 gene and a nucleic acid molecule which down regulates expression of a neutrite growth inhibitor gene (NGO). The nucleic acid may be an endolytic nucleic acid cleaving a RNA molecule possessing an NCH motif, a G-leaver (cleaving RNA with a NYN motif) or an amberzyme (cleaving RNA with an NGN triplet), a zincyme (cleaving RNA with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA of CD20 in the presence of a divalent cation that is preferably Mg^{2+} . Furthermore, it may be contacted with a cell to reduce CD20 activity of the cell and treat a patient having a condition associated with the level of CD20. The treatment may further comprise the use of one or more therapies. In particular, the CD20 targeting nucleic acid may be used to treat lymphoma, leukemia, B-cell lymphoma, low-grade or follicular non-Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic leukemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma, immune thrombocytopenia, and inflammatory arthropathy. The NGO-targeting nucleic acid is used to cleave RNA of the NGO gene in the presence of a divalent cation that is preferably Mg^{2+} . Furthermore, the nucleic acid may be contacted with a cell to reduce NGO activity of the cell and treat a patient having a condition associated with the level of NGO. The treatment may further comprise the use of one or more therapies. In particular, the NGO-targeting nucleic acid may be used to treat central nervous system (CNS) injury and cerebrovascular accident (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS), chemotherapeutic-induced neuropathy, amyotrophic lateral sclerosis (ALS), Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jacob disease, muscular dystrophy, and/or other neurodegenerative disease states which respond to the modulation of NGO expression. The present sequence is a substrate sequence for a nucleic acid of the invention based on the human NGOO sequence

SD Sequence 38 BP; 8 A; 8 C; 10 G; 0 T; 12 U; 0 Other;

Query Match	Score	DB	Length
78.4%	29.8	4	38

Best Local Similarity 93.9%; Pred. No. 0.0032;
Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 2 CUGCAUUCUGAUGAGGCCGUTUAGGCCGAAAAAU 34
|||||
D6 2 CUGCAUUCUGAUGAGGCCGUTUAGGCCGAAAAAU 34

Db 2 CUGCAUUCUGAUGAGGCCGUAAGGCCGAUAU 34

```

RESULT 34
ABK05109
ID    ABK05109 standard; RNA; 38 BP

```

AC ABK05109

DT 12-MAR-2002 (first entry)

DE Human NOGO Inozyme substrate sequence #586

KM Human; antisense therapy; cyostatic; antiinflammatory; haemostatic,
KM chemoprotective; nootropic; neuroprotective; antiparkinsonian;
KM muscular; CD20, neurite growth inhibitor gene, NOGO, hammerhead ribozyme
DNAAzyme; lipozyme; G-cleaver; amebicyme; zinzyme; lymphoma; leukaemia;
KM B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
KM human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
KM HCM; immunocytoemia; IMC; immune thrombocytopenia; stroke; dementia;
KM Inflammatory arthropathy; central nervous system injury;
KM cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
KM chemoreceptor-induced neuropathy; aneurysmal lateral sclerosis; ALS;
KM Parkinson's disease; ataxia; Huntington's disease; substrate sequence;
KM Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease

OS Homo sapiens.

OS Synthetic.

PN W0200159103-A2

PD 16-AUG-2001

PF 09-FEB-2001; 2001WO-US004273.

PR 11-FEB-2000; 2000US-0181797P.

PR 06-MAR-2000; 2000US-0187128P.

PA (RIBO-) RIBOZYME PHARM INC.

PA (MCSW/) MCSWIGGEN J.

XX

XX

XX

PT constructs, which down regulate expression of

PT central nervous system

PS Claim 89; Page 87; 200pp; English

CC The invention relates to a nucleic acid sequence.

regulate expression of a neurite growth inhibitor gene (NGO). The nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a DNAzyme) an inozyme (an endolytic nucleic acid cleaving a RNA molecule possessing an NCR motif), a G-cleaver (cleaving RNA with a NNN motif) or an amberzyme (cleaving RNA with an NNN triplet), a zincyme (cleaving RNA with a YGY motif). The CD20-targeting nucleic acid is used to cleave RNA of CD20 in the presence of a divalent cation that is preferably Mg^{2+} . Furthermore, it may be contacted with a cell to reduce CD20 activity of the cell and treat a patient having a condition associated with the level of CD20. The treatment may further comprise the use of one or more therapies. In particular, the CD20 targeting nucleic acid may be used to treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma, immune thrombocytopenia, and inflammatory arthropathy. The NGO-targeting nucleic acid is used to cleave RNA of the NGO gene in the presence of a divalent cation that is preferably Mg^{2+} . Furthermore, the nucleic acid may be contacted with a cell to reduce NGO activity of the cell and treat a patient having a condition associated with the level of NGO. The treatment may further comprise the use of one or more therapies. In particular, the NGO-targeting nucleic acid may be used to treat central nervous system (CNS) injury and cerebrovascular accident (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS), chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS), Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob disease, muscular dystrophy, and/or other neurodegenerative disease states which respond to the modulation of NGO expression. The present sequence is a substrate sequence for a nucleic acid of the invention based on the human NGO sequence

SQ Sequence 38 BP; 13 A; 6 C; 10 G; 0 T; 8 U; 1 Other;

Query Match	Score	DB	Length
78.4%	29.8	4	38

Matches 31; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 GGAUUCUGAGGCGGUAAGCGGAAAAAUCAG 37

Db 4 GAAACUGAGGCGGUAAGCGGAAAUUCAG 37

Db 4 GAAACUGAUGAGGCCGUGAGGCCGANAUAUCAG 37

RESULT 35

ACN26108
ID ACN26108 standard; RNA; 38 BP.
XX
XX ACN26108;
AC
XX
DT 22-APR-2004 (first entry)
XX
XX MNV minus strand Hammerhead Ribozyme SEQ ID NO 26124.
DE
XX
XX MNV; West Nile Virus; antiinflammatory; cytotatic; hepatotropic;
KM virucide; neuroprotective; antibacterial; replication; pancreatitis;
KM encephalitis; myocarditis; meningitis; infection; hepatitis;
KM liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;
KM Amberzyme; Zinzyme; ss.
XX
XX West Nile Virus.
OS
XX
XX WO200268637-A2.
PN
XX
XX 06-SEP-2002.
PD
XX
XX 19-OCT-2001; 2001WO-US048350.
PF
XX
XX 20-OCT-2000; 2000US-0242411P.
PR
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGEN J A.
XX
XX Blatt L, Mcswigen JA;
PI
XX
XX WPI; 2002-706994/76.
DR
XX
XX New nucleic acid molecule that modulates replication of West Nile Virus
PT (MNV), useful for treating a condition related to MNV infection e.g.
PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
PS
XX
XX Claim 24; SEQ ID NO 26124; 495bp; English.
XX
XX The invention relates to nucleic acid molecules that modulate replication
CC of the West Nile Virus (MNV). The nucleic acid molecules are useful for
CC treating a condition related to MNV infection e.g. pancreatitis,
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
CC molecule is selected from the group of ribozymes consisting of
CC Hammerhead, Inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyme. The
CC nucleic acid molecules further comprise at least five ribose residues, at
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC least three of the 5' terminal nucleotides and a 3' end modification of a
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC in the specification. The present sequence is that of a nucleic acid
CC molecule of the invention
XX
XX
XX Sequence 38 BP; 13 A; 7 C; 13 G; 0 T; 5 U; 0 Other;
SQ
Query Match 78.4%; Score 29.8; DB 6; Length 38;
Best Local Similarity 93.9%; Pred. No. 0.0032;
Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 6 AAUUCGUAUGAGCGCCGUAAGCCGAAAUUACAG 38
DB 6 AAACUGAUGAGCGCCGUAAGCCGAAAUUACAG 38

RESULT 36
ACN27859
ID ACN27859 standard; RNA; 38 BP.
XX
XX ACN27859;
AC
XX
XX 22-APR-2004 (first entry)
DT
XX

DE MNV minus strand Hammerhead Ribozyme SEQ ID NO 27875.
XX
XX MNV; West Nile Virus; antiinflammatory; cytotatic; hepatotropic;
KM virucide; neuroprotective; antibacterial; replication; pancreatitis;
KM encephalitis; myocarditis; meningitis; infection; hepatitis;
KM liver failure; cancer; cirrhosis; Hammerhead; Inozyme; DNAzyme;
KM Amberzyme; Zinzyme; ss.
XX
XX West Nile Virus.
OS
XX
XX WO200268637-A2.
PN
XX
XX 06-SEP-2002.
PD
XX
XX 19-OCT-2001; 2001WO-US048350.
PF
XX
XX 20-OCT-2000; 2000US-0242411P.
PR
XX
XX (RIBO-) RIBOZYME PHARM INC.
PA (BLAT/) BLATT L.
PA (MCSW/) MCSWIGEN J A.
XX
XX Blatt L, Mcswigen JA;
PI
XX
XX WPI; 2002-706994/76.
DR
XX
XX New nucleic acid molecule that modulates replication of West Nile Virus
PT (MNV), useful for treating a condition related to MNV infection e.g.
PT pancreatitis, meningitis, hepatocellular carcinoma or cirrhosis.
PS
XX
XX Claim 24; SEQ ID NO 27875; 495bp; English.
XX
XX The invention relates to nucleic acid molecules that modulate replication
CC of the West Nile Virus (MNV). The nucleic acid molecules are useful for
CC treating a condition related to MNV infection e.g. pancreatitis,
CC encephalitis, myocarditis, meningitis, neurologic infection, hepatitis,
CC liver failure, hepatocellular carcinoma or cirrhosis. The nucleic acid
CC molecule is selected from the group of ribozymes consisting of
CC Hammerhead, Inozyme, G-cleaver, DNAzyme, Amberzyme and Zinzyme. The
CC nucleic acid molecules further comprise at least five ribose residues, at
CC least ten 2'-O-methyl modifications, phosphorothioate linkages on at
CC least three of the 5' terminal nucleotides and a 3' end modification of a
CC 3'-3' inverted abasic moiety. Nucleic acid molecules SEQ ID NO 1 to 37080
CC are claimed; however, SEQ ID NO 2194-2206 and 17502-17514 are not given
CC in the specification. The present sequence is that of a nucleic acid
CC molecule of the invention
XX
XX
XX Sequence 38 BP; 14 A; 9 C; 9 G; 0 T; 6 U; 0 Other;
SQ
Query Match 78.4%; Score 29.8; DB 6; Length 38;
Best Local Similarity 93.9%; Pred. No. 0.0032;
Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 5 CAUUCGUAUGAGCGCCGUAAGCCGAAAUUACAG 37
DB 5 CAUUCGUAUGAGCGCCGUAAGCCGAAAUUACAG 37

RESULT 37
ACD50588
ID ACD50588 standard; RNA; 38 BP.
XX
XX ACD50588;
AC
XX
XX 23-SEP-2003 (first entry)
DT
XX
XX

HBV hammerhead ribozyme sequence #105.
DE
XX
XX Nucleic acid molecule; Hepatitis C virus; HCV; Hepatitis B virus; HBV;
KM RNA stability; RNA expression; RNA synthesis; antisense;
KM enzymatic nucleic acid; hammerhead ribozyme; DNAzyme; inozyme; zinzyme;
KM amberzyme; G-cleaver ribozyme; decoy molecule; aptamer;
KM HBV reverse transcriptase; Enhancer I region; viral replication;

KW degenerative; disease state; HBV infection; HCV infection; cirrhosis;
KM liver failure; hepatocellular carcinoma; hepatotropic; cytostatic;
KM vincide; antiinflammatory; ss.

OS Hepatitis B virus.

PN WO200281494-A1.

PD 17-OCT-2002.

PF 26-MAR-2002; 2002WO-US009187.

PR 26-MAR-2001; 2001US-00817879.

PR 08-JUN-2001; 2001US-00877478.

PR 08-JUN-2001; 2001US-0296876P.

PR 24-OCT-2001; 2001US-0335059P.

PR 05-DEC-2001; 2001US-0337055P.

XX (RIBO-) RIBOZYME PHARM INC.

PA (BLAT/) BLAT L.

PA (MACE/) MACEJAK D.

PA (MCSW/) MCSWIGEN J.

PA (MORR/) MORRISSEY D.

PA (PAVC/) PAVCO P.

PA (LEBP/) LEE P.

PA (DRAP/) DRAPER K.

PA (ROBE/) ROBERTS E.

XX Blact L, Macejak D, Mcswigen J, Morrissey D, Pavco P, Lee P,

PI Draper K, Roberts E;

XX WPI; 2003-229207/22.

XX Novel compound useful for treating cirrhosis, liver failure,

PT hepatocellular carcinoma, or condition associated with hepatitis C virus

PT infection.

XX Example 1; Page 138; 387pp; English.

XX The present invention relates to nucleic acid molecules which modulate

CC the synthesis, expression and/or stability of Hepatitis C virus (HCV) or

CC Hepatitis B virus (HBV) RNA. The nucleic acid molecules include antisense

CC and enzymatic nucleic acids such as hammerhead ribozymes, DNazymes,

CC inozymes, zinczymes, amberyzymes, and G-cleaver ribozymes. Also disclosed

CC are nucleic acid decoy molecules and aptamers that bind to HBV reverse

CC transcriptase and/or HBV reverse transcriptase primer sequences, as well

CC as oligonucleotides that specifically bind the Enhancer 1 region of HBV

CC DNA. The nucleic acids may be used to modulate the expression of HBV

CC genes and HBV viral replication. Also disclosed is a method for screening

CC compounds and/or potential therapies directed against HBV. The compounds

CC that modulate the expression and/or replication of HCV. The compounds and

CC methods of the invention are useful for the treatment of degenerative and

CC disease states related to HBV and HCV infection, replication and gene

CC expression such as cirrhosis, liver failure, and hepatocellular

CC carcinoma. The present sequence represents one of the HBV ribozyme,

CC inozyme, G-cleaver, zinczyme, DNazyme or amberyzyme sequences disclosed in

CC the present invention

XX Sequence 38 BP; 11 A; 8 C; 13 G; 0 T; 6 U; 0 Other;

XX

Query Match 78.4%; Score 29.8; DB 8; Length 38;

Best Local Similarity 93.9%; Pred. No. 0.0032;

Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CC 1 CCUGCAUUCUGAUGAGCGCCGUTAGCGCGAAGAA 33

CC 1 CCUGGAUUCUGAUGAGCGCCGUTAGCGCGAAGAA 33

XX RESULT 38

ADL56345

ID ADL56345 standard; RNA; 38 BP.

AC ADL56345;

XX 20-MAY-2004 (first entry)

XX Human PKR ribozyme sequence #809.

XX antisense oligonucleotide; neurite growth inhibitor; NOGO;

XX prostaglandin D2 receptor; PTGDR; Ikappab kinase; IKK;

XX protein kinase PKR; cerebrovascular accident;

XX central nervous system injury; CNS injury; spinal cord injury; cancer;

XX melanoma; lymphoma; glioma; inflammatory disease; rheumatoid arthritis;

XX osteoarthritis; asthma; Crohn's disease; diabetes; obesity;

XX autoimmune disease; lupus; multiple sclerosis; transplant rejection;

XX graft rejection; ischaemia; reperfusion; glomerulonephritis; sepsis;

XX allergy; asthma; allergic rhinitis; atopic dermatitis; PKR ribozyme;

XX substrate; ss; human.

XX Homo sapiens.

XX WO200281628-A2.

XX 17-OCT-2002.

XX 03-APR-2002; 2002WO-US010512.

XX 05-APR-2001; 2001US-00827395.

XX 29-MAY-2001; 2001US-0294412P.

XX 28-AUG-2001; 2001US-0315315P.

XX (RIBO-) RIBOZYME PHARM INC.

XX Blact L, Chowrira B, Haeblerl P, Mcswigen J, Fosnaugh K;

XX WPI; 2003-058513/05.

XX Novel enzymatic nucleic acid that down-regulates expression of neurite

PT growth inhibitor receptor, prostaglandin D2 receptor, Ikappab kinase or

PT protein kinase PKR genes, for treating cancer and inflammatory disease.

XX Claim 57; SEQ ID NO 9878; 317pp; English.

XX The invention comprises nucleic acids (e.g. antisense oligonucleotides)

CC that down regulate the expression or inhibit the function of a receptor

CC for a neurite growth inhibitor, NOGO, prostaglandin D2 receptor (PTGDR),

CC Ikappab kinase (IKK), or protein kinase PKR. The nucleic acids of the

CC invention are useful for treating: cerebrovascular accident, central

CC nervous system (CNS) injury, spinal cord injury, cancer (e.g. melanoma,

CC lymphoma or glioma), inflammatory disease (e.g. rheumatoid arthritis,

CC osteoarthritis or asthma), Crohn's disease, diabetes, obesity, autoimmune

CC disease, lupus, multiple sclerosis, transplant/graft rejection,

CC ischaemia/reperfusion injury, glomerulonephritis, sepsis, and allergic

CC conditions (e.g. asthma, allergic rhinitis or atopic dermatitis). The

CC nucleic acids of the invention are also useful for down-regulating the

CC expression of a target gene and as a diagnostic tool to examine genetic

CC drifts and mutations within diseased cells or to detect the presence of a

CC target RNA in a cell. The present RNA sequence represents a human PKR

CC ribozyme sequence.

XX Sequence 38 BP; 13 A; 8 C; 11 G; 0 T; 5 U; 1 Other;

XX

Query Match 78.4%; Score 29.8; DB 11; Length 38;

Best Local Similarity 91.2%; Pred. No. 0.0032;

Matches 31; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CC 4 GCAUUCUGAUGAGCGCCGUTAGCGCGAAGAAUACG 37

CC 4 GCAAAUCUGAUGAGCGCCGUTAGCGCGAANAACG 37

XX RESULT 39

ADM60513

ID ADM60513 standard; RNA; 38 BP.

AC ADM60513;
 XX
 DT 03-JUN-2004 (first entry)
 XX
 DE Hepatitis B virus (HBV) enzymatic nucleic acid #105.
 XX
 KW Hepatitis B virus; HBV; ss; enzymatic nucleic acid; RNA cleavage;
 KW hepatitis B virus infection; hepatitis; hepatocellular carcinoma;
 KW cirrhosis; liver failure; lamivudine; interferon; genetic drift;
 KW virocid; hepatotropic; antiinflammatory; cytosolic.
 XX
 OS Hepatitis B virus.
 XX
 PN US2004054156-A1.
 XX
 PD 18-MAR-2004.
 XX
 PF 15-JAN-2003; 2003US-00342902.
 XX
 PR 14-MAY-1992; 92US-00882712.
 PR 07-FEB-1994; 94US-00193627.
 PR 08-NOV-1999; 99US-00436430.
 PR 20-MAR-2000; 2000US-00531025.
 PR 09-AUG-2000; 2000US-00636385.
 PR 24-OCT-2000; 2000US-00696347.
 PR 08-JUN-2001; 2001US-00877478.
 XX
 PA (DRAP/) DRAPER K.
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGEN J A.
 PA (MORR/) MORRISSEY D.
 XX
 PI Draper K, Blatt L, Mcswigen JA, Morrissey D;
 DR
 DR WPI: 2004-247781/23.
 XX
 PT Novel enzymatic nucleic acid molecule such as DNAzymes and inozymes
 PT specifically cleaving RNA derived from hepatitis B virus and comprising
 PT one or more binding arms, useful for treating hepatitis and cirrhosis.
 XX
 PS Disclosure; SEQ ID NO 2647; 122bp; English.
 XX
 CC The invention relates to an enzymatic nucleic acid molecule that
 CC specifically cleaves RNA derived from hepatitis B virus (HBV) and
 CC comprising one or more binding arms, without requiring the presence of a
 CC 2'-OH group within the molecule for activity. The nucleic acids are
 CC useful for treating hepatitis B virus infection, hepatitis,
 CC hepatocellular carcinoma, cirrhosis and liver failure, either alone or in
 CC combination with other therapies such as lamivudine and interferons. The
 CC nucleic acids are useful as diagnostic tools to examine genetic drift and
 CC mutations within diseased cells, for detecting the presence of HBV RNA in
 CC a cell, for the study of RNA and for down-regulating gene expression of
 CC target genes in bacterial, fungal, viral, plant or mammalian cells. This
 CC sequence represents an enzymatic nucleic acid molecule which cleaves HBV
 CC RNA of the invention. Note: The sequence data for this patent is also
 CC available in electronic format from USPTO at
 CC seqdata.uspto.gov/sequence.html.
 CC
 SQ Sequence 38 BP; 11 A; 8 C; 13 G; 0 T; 6 U; 0 Other;
 XX
 XX
 Query Match 78.4%; Score 29.8; DB 12; Length 38;
 Best Local Similarity 93.9%; Pred. No. 0.0032;
 Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 CCUGCAUCUGAUGAGCCGUAAGCCGAAAAA 33
 1 CCUGCAUCUGAUGAGCCGUAAGCCGAAAAA 33
 DB
 RESULT 40
 ABX02648
 ID ABX02648 standard; RNA; 36 BP.

AC ABX02648;
 XX
 DT 23-DEC-2002 (first entry)
 XX
 DE HCV hammerhead ribozyme #821 for Hepatitis C virus substrate #821.
 XX
 KW Enzymatic nucleic acid; RNA cleavage; Hepatitis C virus infection;
 KW HCV ribozyme; HCV expression; HCV replication; cirrhosis; virocid;
 KW liver failure; hepatocellular carcinoma; HCV infection; drug therapy;
 KW type I interferon; interferon alpha; interferon beta; cytosolic;
 KW interferon gamma; consensus interferon; hepatotropic; antiinflammatory;
 KW hammerhead ribozyme; HH ribozyme; ss.
 XX
 OS Hepatitis C virus.
 XX
 PN US2002082225-A1.
 XX
 PD 27-JUN-2002.
 XX
 PR 23-MAR-1999; 99US-00274553.
 XX
 PR 23-MAR-1999; 99US-00274553.
 XX
 PA (BLAT/) BLATT L.
 PA (MCSW/) MCSWIGEN J A.
 PA (ROBE/) ROBERTS B.
 PA (PAVC/) PAVCO P A.
 PA (MACE/) MACEJACK D.
 XX
 PI Blatt L, Mcswigen JA, Roberts B, Pavco PA, Macejack D;
 DR
 DR WPI: 2002-617759/66.
 XX
 PT New ribozymes targeting RNA derived from hepatitis C virus inhibit viral
 PT replication and are useful to treat hepatitis C virus infections and
 PT cirrhosis, liver failure or hepatocellular carcinoma.
 XX
 PS Claim 8; Page 45; 80bp; English.
 XX
 CC The present invention relates to enzymatic nucleic acids which
 CC specifically cleave RNA derived from Hepatitis C virus (HCV). The
 CC enzymatic nucleic acid or ribozyme is in a hammerhead (HH) or hairpin
 CC (HP) motif where the binding arms comprise sequences complementary to one
 CC of the substrate sequences defined in the specification. The HCV
 CC ribozymes are useful for modulating the expression and/or replication of
 CC HCV. They can be used to treat cirrhosis, liver failure and/or
 CC hepatocellular carcinoma. The HCV ribozymes are also useful for treating
 CC a condition associated with HCV infection in conjunction with one or more
 CC other drug therapies, particularly type I interferon, especially
 CC interferon alpha, beta or gamma or consensus interferon. The present
 CC sequence represents a HCV hammerhead (HH) ribozyme. Note: Some of the
 CC sequence data for this patent did not form part of the printed
 CC specification. The complete sequence data for this patent was obtained in
 CC electronic format directly from the USPTO web site at
 CC seqdata.uspto.gov/patidentry.html
 CC
 SQ Sequence 36 BP; 9 A; 9 C; 12 G; 0 T; 6 U; 0 Other;
 XX
 XX
 Query Match 77.9%; Score 29.6; DB 6; Length 36;
 Best Local Similarity 88.9%; Pred. No. 0.0039;
 Matches 32; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 2 CUGCAUCUGAUGAGCCGUAAGCCGAAAAAUCAG 37
 1 CCGCAUCUGAUGAGCCGUAAGCCGAAACGUCAG 36
 DB
 Search completed: May 13, 2005, 17:06:07
 Job time : 282.173 secs

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OM nucleic - nucleic search, using sw model

Run on: May 13, 2005, 16:59:31 ; Search time 93.9636 Seconds
(without alignments)
661.730 Million cell updates/sec

Title: US-09-927-046-2332
Perfect score: 38
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 1330268

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Issued Patents NA:
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5: /cgn2_6/prodata/1/ina/ECTUS_COMB_seq:*
6: /cgn2_6/prodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31.2	82.1	38	4	US-09-371-772B-8898 Sequence 8898, Ap
2	31.2	82.1	38	4	US-09-371-772B-9385 Sequence 9385, Ap
3	30.8	81.1	38	4	US-09-371-772B-7472 Sequence 7472, Ap
4	30.8	81.1	38	4	US-09-371-772B-8673 Sequence 8673, Ap
5	30.6	80.5	38	4	US-09-371-772B-9574 Sequence 9574, Ap
6	30.4	80.0	38	4	US-09-371-772B-9413 Sequence 9413, Ap
7	30.4	80.0	38	4	US-09-371-772B-10563 Sequence 10563, A
8	30.2	79.5	38	4	US-09-371-772B-8143 Sequence 8143, A
9	30.2	79.5	38	4	US-09-371-772B-7526 Sequence 7526, Ap
10	30	78.9	38	4	US-09-371-772B-7666 Sequence 7666, Ap
11	30	78.9	38	4	US-09-371-772B-9539 Sequence 9539, Ap
12	29.8	78.4	38	4	US-09-371-772B-8240 Sequence 8240, Ap
13	29.8	78.4	38	4	US-09-371-772B-8345 Sequence 8345, Ap
14	29.8	78.4	38	4	US-09-371-772B-8530 Sequence 8530, Ap
15	29.6	77.9	38	4	US-09-371-772B-8913 Sequence 8913, Ap
16	29.4	77.4	38	4	US-09-371-772B-7656 Sequence 7656, Ap
17	29.4	77.4	38	4	US-09-371-772B-7863 Sequence 7863, Ap
18	29.4	77.4	38	4	US-09-371-772B-8422 Sequence 8422, Ap
19	29.4	77.4	38	4	US-09-371-772B-8953 Sequence 8953, Ap
20	29.4	77.4	38	4	US-09-371-772B-9507 Sequence 9507, Ap
21	29.4	77.4	38	4	US-09-371-772B-9559 Sequence 9559, Ap
22	29.4	77.4	38	4	US-09-371-772B-11300 Sequence 11300, A
23	29.2	76.8	38	1	US-08-373-124A-1754 Sequence 1754, Ap
24	29.2	76.8	38	1	US-08-435-62B-1754 Sequence 1754, Ap
25	29.2	76.8	38	4	US-09-371-772B-8298 Sequence 8298, Ap
26	29.2	76.8	38	4	US-09-371-772B-8707 Sequence 8707, Ap
27	29.2	76.8	38	4	US-09-371-772B-9621 Sequence 9621, Ap

28	29	76.3	38	4	US-09-371-772B-8786 Sequence 8786, Ap
29	29	76.3	38	4	US-09-371-772B-10855 Sequence 10855, A
30	29	76.3	38	4	US-09-371-772B-13264 Sequence 13264, A
31	28.8	75.8	38	4	US-09-371-772B-7533 Sequence 7533, Ap
32	28.8	75.8	38	4	US-09-371-772B-8047 Sequence 8047, Ap
33	28.8	75.8	38	4	US-09-371-772B-8328 Sequence 8328, Ap
34	28.8	75.8	38	4	US-09-371-772B-10400 Sequence 10400, A
35	28.8	75.8	38	4	US-09-371-772B-10648 Sequence 10648, A
36	28.8	75.8	38	4	US-09-371-772B-11024 Sequence 11024, A
37	28.8	75.8	38	4	US-09-371-772B-12223 Sequence 12223, A
38	28.8	75.8	38	4	US-09-371-772B-12495 Sequence 12495, A
39	28.8	75.8	38	4	US-09-371-772B-13894 Sequence 13894, A
40	28.6	75.3	38	4	US-09-371-772B-7626 Sequence 7626, Ap
41	28.6	75.3	38	4	US-09-371-772B-8158 Sequence 8158, Ap
42	28.6	75.3	38	4	US-09-371-772B-8336 Sequence 8336, Ap
43	28.6	75.3	38	4	US-09-371-772B-8763 Sequence 8763, Ap
44	28.6	75.3	38	4	US-09-371-772B-9259 Sequence 9259, Ap
45	28.6	75.3	38	4	US-09-371-772B-9546 Sequence 9546, Ap
46	28.4	74.7	38	4	US-09-371-772B-7180 Sequence 7180, Ap
47	28.4	74.7	38	4	US-09-371-772B-7386 Sequence 7386, Ap
48	28.4	74.7	38	4	US-09-371-772B-7805 Sequence 7805, Ap
49	28.4	74.7	38	4	US-09-371-772B-7830 Sequence 7830, Ap
50	28.4	74.7	38	4	US-09-371-772B-7921 Sequence 7921, Ap
51	28.4	74.7	38	4	US-09-371-772B-8416 Sequence 8416, Ap
52	28.4	74.7	38	4	US-09-371-772B-8819 Sequence 8819, Ap
53	28.4	74.7	38	4	US-09-371-772B-10071 Sequence 10071, A
54	28.4	74.7	38	4	US-09-371-772B-10469 Sequence 10469, A
55	28.4	74.7	38	4	US-09-371-772B-10647 Sequence 10647, A
56	28.4	74.7	38	4	US-09-371-772B-10873 Sequence 10873, A
57	28.4	74.7	38	4	US-09-371-772B-12392 Sequence 12392, A
58	28.2	74.2	36	1	US-08-319-492B-259 Sequence 259, App
59	28.2	74.2	38	4	US-09-371-772B-7448 Sequence 7448, Ap
60	28.2	74.2	38	4	US-09-371-772B-7475 Sequence 7475, Ap
61	28.2	74.2	38	4	US-09-371-772B-7494 Sequence 7494, Ap
62	28.2	74.2	38	4	US-09-371-772B-7623 Sequence 7623, Ap
63	28.2	74.2	38	4	US-09-371-772B-7859 Sequence 7859, Ap
64	28.2	74.2	38	4	US-09-371-772B-7880 Sequence 7880, Ap
65	28.2	74.2	38	4	US-09-371-772B-7888 Sequence 7888, Ap
66	28.2	74.2	38	4	US-09-371-772B-7898 Sequence 7898, Ap
67	28.2	74.2	38	4	US-09-371-772B-8004 Sequence 8004, Ap
68	28.2	74.2	38	4	US-09-371-772B-8008 Sequence 8008, Ap
69	28.2	74.2	38	4	US-09-371-772B-8044 Sequence 8044, Ap
70	28.2	74.2	38	4	US-09-371-772B-8178 Sequence 8178, Ap
71	28.2	74.2	38	4	US-09-371-772B-8312 Sequence 8312, Ap
72	28.2	74.2	38	4	US-09-371-772B-8853 Sequence 8853, Ap
73	28.2	74.2	38	4	US-09-371-772B-8917 Sequence 8917, Ap
74	28.2	74.2	38	4	US-09-371-772B-9115 Sequence 9115, Ap
75	28.2	74.2	38	4	US-09-371-772B-9761 Sequence 9761, Ap
76	28.2	74.2	38	4	US-09-371-772B-9829 Sequence 9829, Ap
77	28.2	74.2	38	4	US-09-371-772B-9895 Sequence 9895, Ap
78	28.2	74.2	38	4	US-09-371-772B-9917 Sequence 9917, A
79	28.2	74.2	38	4	US-09-371-772B-10721 Sequence 10721, A
80	28.2	74.2	38	4	US-09-371-772B-12293 Sequence 12293, A
81	28.2	74.2	38	4	US-09-371-772B-13861 Sequence 13861, A
82	28	73.7	38	4	US-09-371-772B-7524 Sequence 7524, Ap
83	28	73.7	38	4	US-09-371-772B-7682 Sequence 7682, Ap
84	28	73.7	38	4	US-09-371-772B-7767 Sequence 7767, Ap
85	28	73.7	38	4	US-09-371-772B-8109 Sequence 8109, Ap
86	28	73.7	38	4	US-09-371-772B-8171 Sequence 8171, Ap
87	28	73.7	38	4	US-09-371-772B-8196 Sequence 8196, Ap
88	28	73.7	38	4	US-09-371-772B-8408 Sequence 8408, Ap
89	28	73.7	38	4	US-09-371-772B-9105 Sequence 9105, Ap
90	28	73.7	38	4	US-09-371-772B-9298 Sequence 9298, Ap
91	28	73.7	38	4	US-09-371-772B-9456 Sequence 9456, Ap
92	28	73.7	38	4	US-09-371-772B-9496 Sequence 9496, Ap
93	28	73.7	38	4	US-09-371-772B-9546 Sequence 9546, Ap
94	28	73.7	38	4	US-09-371-772B-9616 Sequence 9616, Ap
95	28	73.7	38	4	US-09-371-772B-9916 Sequence 9916, Ap
96	28	73.7	38	4	US-09-371-772B-10021 Sequence 10021, A
97	28	73.7	38	4	US-09-371-772B-10059 Sequence 10059, A
98	28	73.7	38	4	US-09-371-772B-10913 Sequence 10913, A
99	28	73.7	38	4	US-09-371-772B-10946 Sequence 10946, A
100	28	73.7	38	4	US-09-371-772B-11279 Sequence 11279, A

ALIGNMENTS

RESULT 1
US-09-371-772B-8898/ Sequence 8898, Application US/09371772B
/ Patent No. 6566127
/ GENERAL INFORMATION:
/ APPLICANT: Ribozyme Pharmaceuticals, Inc./ APPLICANT: Pavco, Pam
/ APPLICANT: McSwigen, Jim
/ APPLICANT: Stinchcomb, Dan
/ APPLICANT: Escobedo, Jaime/ TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
/ FILE REFERENCE: MBH00,876-J (237/198)
/ CURRENT APPLICATION NUMBER: US/09/371,772B/ PRIOR FILING DATE: 1999-08-10
/ PRIOR APPLICATION NUMBER: US 60/005,974
/ PRIOR FILING DATE: 1995-10-26/ PRIOR APPLICATION NUMBER: US 08/584,040
/ NUMBER OF SEQ ID NOS: 14225
/ SOFTWARE: PatentIn version 3.0/ SEQ ID NO 8898
/ LENGTH: 38
/ TYPE: RNA
/ ORGANISM: Artificial Sequence/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid

US-09-371-772B-8898

Query Match
Best Local Similarity 82.1%; Score 31.2; DB 4; Length 38;
Matches 33; Conservative 0; Mismatches 3; Indels 0; Gaps 0;QY 1 CCUGCAUCUGAUGAGCGCGUUGAGCCGAAAAAUAUC 36
DB 1 CCUGCAUCUGAUGAGCGCGUUGAGCCGAAAAAUAUC 36RESULT 2
US-09-371-772B-9385/ Sequence 9385, Application US/09371772B
/ Patent No. 6566127
/ GENERAL INFORMATION:
/ APPLICANT: Ribozyme Pharmaceuticals, Inc./ APPLICANT: Pavco, Pam
/ APPLICANT: McSwigen, Jim
/ APPLICANT: Stinchcomb, Dan
/ APPLICANT: Escobedo, Jaime/ TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
/ FILE REFERENCE: MBH00,876-J (237/198)
/ CURRENT APPLICATION NUMBER: US/09/371,772B/ PRIOR FILING DATE: 1999-08-10
/ PRIOR APPLICATION NUMBER: US 60/005,974
/ PRIOR FILING DATE: 1995-10-26/ PRIOR APPLICATION NUMBER: US 08/584,040
/ NUMBER OF SEQ ID NOS: 14225
/ SOFTWARE: PatentIn version 3.0/ SEQ ID NO 9385
/ LENGTH: 38
/ TYPE: RNA
/ ORGANISM: Artificial Sequence/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid

US-09-371-772B-9385

Query Match 82.1%; Score 31.2; DB 4; Length 38;

Best Local Similarity 91.7%; Pred. No. 4.9e-05;
Matches 33; Conservative 0; Mismatches 3; Indels 0; Gaps 0;QY 1 CCUGCAUCUGAUGAGCGCGUUGAGCCGAAAAAUAUC 36
DB 1 CCUGCAUCUGAUGAGCGCGUUGAGCCGAAAAAUAUC 36RESULT 3
US-09-371-772B-7472/ Sequence 7472, Application US/09371772B
/ Patent No. 6566127
/ GENERAL INFORMATION:
/ APPLICANT: Ribozyme Pharmaceuticals, Inc./ APPLICANT: Pavco, Pam
/ APPLICANT: McSwigen, Jim
/ APPLICANT: Stinchcomb, Dan/ TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
/ FILE REFERENCE: MBH00,876-J (237/198)
/ CURRENT APPLICATION NUMBER: US/09/371,772B/ PRIOR FILING DATE: 1999-08-10
/ PRIOR APPLICATION NUMBER: US 60/005,974
/ PRIOR FILING DATE: 1995-10-26/ PRIOR APPLICATION NUMBER: US 08/584,040
/ NUMBER OF SEQ ID NOS: 14225
/ SOFTWARE: PatentIn version 3.0/ SEQ ID NO 7472
/ LENGTH: 38
/ TYPE: RNA
/ ORGANISM: Artificial Sequence/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid

US-09-371-772B-7472

Query Match
Best Local Similarity 81.1%; Score 30.8; DB 4; Length 38;
Matches 32; Conservative 0; Mismatches 2; Indels 0; Gaps 0;QY 2 CUGCAUCUGAUGAGCGCGUUGAGCCGAAAAAUAUC 35
DB 2 CUGCAUCUGAUGAGCGCGUUGAGCCGAAAAAUAUC 35RESULT 4
US-09-371-772B-8673/ Sequence 8673, Application US/09371772B
/ Patent No. 6566127
/ GENERAL INFORMATION:
/ APPLICANT: Ribozyme Pharmaceuticals, Inc./ APPLICANT: Pavco, Pam
/ APPLICANT: McSwigen, Jim
/ APPLICANT: Stinchcomb, Dan
/ APPLICANT: Escobedo, Jaime/ TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
/ FILE REFERENCE: MBH00,876-J (237/198)
/ CURRENT APPLICATION NUMBER: US/09/371,772B/ PRIOR FILING DATE: 1999-08-10
/ PRIOR APPLICATION NUMBER: US 60/005,974
/ PRIOR FILING DATE: 1995-10-26/ PRIOR APPLICATION NUMBER: US 08/584,040
/ NUMBER OF SEQ ID NOS: 14225
/ SOFTWARE: PatentIn version 3.0/ SEQ ID NO 8673
/ LENGTH: 38
/ TYPE: RNA
/ ORGANISM: Artificial Sequence/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid

Query Match 81.1%; Score 30.8; DB 4; Length 38;

US-09-371-772B-8673

Query Match 81.1%; Score 30.8; DB 4; Length 38;
Best Local Similarity 94.1%; Pred. No. 7.5e-05;
Matches 32; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCUGCAUUCGAGGCGGUAAGCCGAAAUU 34
DB 1 CCUGCAUUCGAGGCGGUAAGCCGAAAUU 34

RESULT 5

US-09-371-772B-9574
Sequence 9574, Application US/09371772B
Patent No. 6566127
GENERAL INFORMATION:
APPLICANT: Ribozyne Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
APPLICANT: MCSwigen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Relating to the Growth of Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MBH00, 876-J (237/198)
CURRENT APPLICATION NUMBER: US/09/371, 772B
CURRENT FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: US 60/005, 974
PRIOR FILING DATE: 1995-10-26
PRIOR APPLICATION NUMBER: US 08/584, 040
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: Patent version 3.0
SEQ ID NO 9574
LENGTH: 38
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-9574

Query Match 80.5%; Score 30.6; DB 4; Length 38;
Best Local Similarity 89.2%; Pred. No. 9.3e-05;
Matches 33; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 CUGCAUUCGAGGCGGUAAGCCGAAAUU 38
DB 2 CUGCAUUCGAGGCGGUAAGCCGAAAUU 38

RESULT 6

US-09-371-772B-9413
Sequence 9413, Application US/09371772B
Patent No. 6566127
GENERAL INFORMATION:
APPLICANT: Ribozyne Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
APPLICANT: MCSwigen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Relating to the Growth of Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MBH00, 876-J (237/198)
CURRENT APPLICATION NUMBER: US/09/371, 772B
CURRENT FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: US 60/005, 974
PRIOR FILING DATE: 1995-10-26
PRIOR APPLICATION NUMBER: US 08/584, 040
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: Patent version 3.0
SEQ ID NO 9413
LENGTH: 38
TYPE: RNA

ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-9413

Query Match 80.0%; Score 30.4; DB 4; Length 38;
Best Local Similarity 96.9%; Pred. No. 0.00012;
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCUGCAUUCGAGGCGGUAAGCCGAAAU 32
DB 1 CCUGCAUUCGAGGCGGUAAGCCGAAAU 32

RESULT 7

US-09-371-772B-10563
Sequence 10563, Application US/09371772B
Patent No. 6566127
GENERAL INFORMATION:
APPLICANT: Ribozyne Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
APPLICANT: MCSwigen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Relating to the Growth of Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MBH00, 876-J (237/198)
CURRENT APPLICATION NUMBER: US/09/371, 772B
CURRENT FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: US 60/005, 974
PRIOR FILING DATE: 1995-10-26
PRIOR APPLICATION NUMBER: US 08/584, 040
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: Patent version 3.0
SEQ ID NO 10563
LENGTH: 38
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-10563

Query Match 80.0%; Score 30.4; DB 4; Length 38;
Best Local Similarity 96.9%; Pred. No. 0.00012;
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 AUCGUAUAGGCGGUAAGCCGAAAUU 38
DB 7 AUCGUAUAGGCGGUAAGCCGAAAUU 38

RESULT 8

US-09-371-772B-8143
Sequence 8143, Application US/09371772B
Patent No. 6566127
GENERAL INFORMATION:
APPLICANT: Ribozyne Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
APPLICANT: MCSwigen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Relating to the Growth of Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MBH00, 876-J (237/198)
CURRENT APPLICATION NUMBER: US/09/371, 772B
CURRENT FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: US 60/005, 974
PRIOR FILING DATE: 1995-10-26
PRIOR APPLICATION NUMBER: US 08/584, 040
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: Patent version 3.0

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; SEQ ID NO 8143
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; US-09-371-772B-8143
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Query Match
Best Local Similarity 79.5%; Score 30.2; DB 4; Length 38;
Best Local Similarity 91.4%; Pred. No. 0.00014;
Matches 32; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY 2 CCUGCAUUCUGAUGAGCCCGUAGGCCGAAAUUACA 36
DB 2 CUACAGUCUGAUGAGCCCGUAGGCCGAAAUUUA 36
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RESULT 9

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US-09-371-772B-7526
; Sequence 7526, Application US/09371772B
; Patent No. 6566127
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; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
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; APPLICANT: McSwigen, Jim
; APPLICANT: Stinchcomb, Dan
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; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; FILE REFERENCE: MBH00, 876-J (237/198)
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; CURRENT APPLICATION NUMBER: US/09/371, 772B
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; PRIOR FILING DATE: 1999-08-10
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; PRIOR APPLICATION NUMBER: US 60/005, 974
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; PRIOR FILING DATE: 1995-10-26
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; PRIOR APPLICATION NUMBER: US 08/584, 040
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; NUMBER OF SEQ ID NOS: 14225
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; SOFTWARE: Patentin version 3.0
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; SEQ ID NO 7526
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; LENGTH: 38
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; TYPE: RNA
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; ORGANISM: Artificial Sequence
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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; US-09-371-772B-7526
```

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Query Match
Best Local Similarity 78.9%; Score 30; DB 4; Length 38;
Best Local Similarity 86.8%; Pred. No. 0.00018;
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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QY 1 CCUGCAUUCUGAUGAGCCCGUAGGCCGAAAUUACA 38
DB 1 CCUAAAUUCUGAUGAGCCCGUAGGCCGAAAUUCCA 38
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RESULT 10

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US-09-371-772B-7766
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; Sequence 7766, Application US/09371772B
; Patent No. 6566127
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; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
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; APPLICANT: McSwigen, Jim
; APPLICANT: Stinchcomb, Dan
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; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
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; FILE REFERENCE: MBH00, 876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371, 772B
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; PRIOR FILING DATE: 1999-08-10
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; PRIOR APPLICATION NUMBER: US 60/005, 974
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; PRIOR FILING DATE: 1995-10-26
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; PRIOR APPLICATION NUMBER: US 08/584, 040
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; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 7766
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; US-09-371-772B-7766
```

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Query Match
Best Local Similarity 78.9%; Score 30; DB 4; Length 38;
Best Local Similarity 86.8%; Pred. No. 0.00018;
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

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QY 1 CCUGCAUUCUGAUGAGCCCGUAGGCCGAAAUUACA 38
DB 1 CCUAAAUUCUGAUGAGCCCGUAGGCCGAAAUUCCA 38
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QY 1 CCUGCAUUCUGAUGAGCCCGUAGGCCGAAAUUACA 38
DB 1 CCUAAAUUCUGAUGAGCCCGUAGGCCGAAAUUCCA 38
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RESULT 11

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US-09-371-772B-9539
; Sequence 9539, Application US/09371772B
; Patent No. 6566127
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; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
```

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; APPLICANT: McSwigen, Jim
; APPLICANT: Stinchcomb, Dan
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; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
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; FILE REFERENCE: MBH00, 876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371, 772B
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; PRIOR FILING DATE: 1999-08-10
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; PRIOR APPLICATION NUMBER: US 60/005, 974
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; PRIOR FILING DATE: 1995-10-26
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; PRIOR APPLICATION NUMBER: US 08/584, 040
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; NUMBER OF SEQ ID NOS: 14225
```

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; SOFTWARE: Patentin version 3.0
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; SEQ ID NO 9539
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; LENGTH: 38
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; TYPE: RNA
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; ORGANISM: Artificial Sequence
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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; US-09-371-772B-9539
```

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Query Match
Best Local Similarity 78.9%; Score 30; DB 4; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.00018;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

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QY 4 GCAUUCUGAUGAGCCCGUAGGCCGAAAUUACA 33
DB 4 GCAUUCUGAUGAGCCCGUAGGCCGAAAUUACA 33
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RESULT 12

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US-09-371-772B-8240
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; Sequence 8240, Application US/09371772B
; Patent No. 6566127
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; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
```

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; APPLICANT: McSwigen, Jim
; APPLICANT: Stinchcomb, Dan
```

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; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
```

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; FILE REFERENCE: MBH00, 876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371, 772B
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; PRIOR FILING DATE: 1999-08-10
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; PRIOR APPLICATION NUMBER: US 08/584, 040
```

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; PRIOR FILING DATE: 1995-10-26
```

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; PRIOR APPLICATION NUMBER: US 08/584, 040
```

```

; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 8240
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-8240

Query Match      78.4%; Score 29.8; DB 4; Length 38;
Best Local Similarity 93.9%; Pred. No. 0.00022;
Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      6 AAUCUGAUGAGGCCGUGAGCCGAAAUCAAG 38
Db      6 AUUCUGAUGAGGCCGUGAGCCGAAAUCAAG 38

RESULT 13
US-09-371-772B-8345
; Sequence 8345, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; PRIOR FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 8345
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-8345

Query Match      78.4%; Score 29.8; DB 4; Length 38;
Best Local Similarity 93.9%; Pred. No. 0.00022;
Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      6 AAUCUGAUGAGGCCGUGAGCCGAAAUCAAG 38
Db      6 AUUCUGAUGAGGCCGUGAGCCGAAAUCAAG 38

RESULT 14
US-09-371-772B-8530
; Sequence 8530, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
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; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; PRIOR FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 8530
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-8530

Query Match      78.4%; Score 29.8; DB 4; Length 38;
Best Local Similarity 93.9%; Pred. No. 0.00022;
Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 CCUGAAUCUGAUGAGGCCGUGAGCCGAAAUU 34
Db      2 CUGAAUCUGAUGAGGCCGUGAGCCGAAAUU 34

RESULT 15
US-09-371-772B-8913
; Sequence 8913, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00,876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; PRIOR FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 8913
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-8913

Query Match      77.9%; Score 29.6; DB 4; Length 38;
Best Local Similarity 88.9%; Pred. No. 0.00027;
Matches 32; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 CCUGAAUCUGAUGAGGCCGUGAGCCGAAAUCA 36
Db      1 CGUGAAGCUGAUGAGGCCGUGAGCCGAAAUCA 36

RESULT 16
US-09-371-772B-7656
; Sequence 7656, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
```

```

; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00, 876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7656
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-7656
```

```

Query Match          77.4%; Score 29.4; DB 4; Length 38;
Best Local Similarity 96.8%; Pred. No. 0.00034;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```

QY 7 AUCUGAUGAGGCCGCUUAGCCGCAAAAUAUCAG 37
Db 7 AACUGAUGAGGCCGCUUAGCCGCAAAAUAUCAG 37
```

```

RESULT 17
US-09-371-772B-7863
; Sequence 7863, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00, 876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7863
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-7863
```

```

Query Match          77.4%; Score 29.4; DB 4; Length 38;
Best Local Similarity 96.8%; Pred. No. 0.00034;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```

QY 6 AAUCUGAUGAGGCCGCUUAGCCGCAAAAUAUCA 36
Db 6 AAACUGAUGAGGCCGCUUAGCCGCAAAAUAUCA 36
```

```

RESULT 18
US-09-371-772B-8422
; Sequence 8422, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
```

```

; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00, 876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8422
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-8422
```

```

Query Match          77.4%; Score 29.4; DB 4; Length 38;
Best Local Similarity 96.8%; Pred. No. 0.00034;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```

QY 7 AUCUGAUGAGGCCGCUUAGCCGCAAAAUAUCAG 37
Db 7 AUCUGAUGAGGCCGCUUAGCCGCAAAAUAUCAG 37
```

```

RESULT 19
US-09-371-772B-8953
; Sequence 8953, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00, 876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371,772B
; CURRENT FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584,040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8953
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-8953
```

```

Query Match          77.4%; Score 29.4; DB 4; Length 38;
Best Local Similarity 96.8%; Pred. No. 0.00034;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```

QY 1 CCUGCAUCUGAUGAGGCCGCUUAGCCGCAAAA 31
Db 1 CCUGCAACUGAUGAGGCCGCUUAGCCGCAAAA 31
```

```

RESULT 20
US-09-371-772B-9507
; Sequence 9507, Application US/09371772B
```

Patent No. 6566127
GENERAL INFORMATION:
APPLICANT: Ribozyne Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
APPLICANT: McSwiggen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MBH00, 876-J (237/198)
CURRENT APPLICATION NUMBER: US/09/371, 772B
CURRENT FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: US 60/005, 974
PRIOR FILING DATE: 1995-10-26
PRIOR APPLICATION NUMBER: US 08/584, 040
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: PatentIn version 3.0
SEQ ID NO 9507
LENGTH: 38
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-9507

Query Match 77.4%; Score 29.4; DB 4; Length 38;
Best Local Similarity 96.8%; Pred. No. 0.00034;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 UCUGAUGAGCGCCGUAUAGCGCGAANAUCAGG 38
Db 8 UCUGAUGAGCGCCGUAUAGCGCGAANAUCAGG 38

RESULT 21
US-09-371-772B-9559
Sequence 9559, Application US/09371772B
Patent No. 6566127
GENERAL INFORMATION:
APPLICANT: Ribozyne Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
APPLICANT: McSwiggen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MBH00, 876-J (237/198)
CURRENT APPLICATION NUMBER: US/09/371, 772B
CURRENT FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: US 60/005, 974
PRIOR FILING DATE: 1995-10-26
PRIOR APPLICATION NUMBER: US 08/584, 040
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: PatentIn version 3.0
SEQ ID NO 9559
LENGTH: 38
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-9559

Query Match 77.4%; Score 29.4; DB 4; Length 38;
Best Local Similarity 96.8%; Pred. No. 0.00034;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 UCUGAUGAGCGCCGUAUAGCGCGAANAUCAGG 38
Db 8 UCUGAUGAGCGCCGUAUAGCGCGAANAUCAGG 38

RESULT 22
US-09-371-772B-11300
Sequence 11300, Application US/09371772B
Patent No. 6566127
GENERAL INFORMATION:
APPLICANT: Ribozyne Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
APPLICANT: McSwiggen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MBH00, 876-J (237/198)
CURRENT APPLICATION NUMBER: US/09/371, 772B
CURRENT FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: US 60/005, 974
PRIOR FILING DATE: 1995-10-26
PRIOR APPLICATION NUMBER: US 08/584, 040
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: PatentIn version 3.0
SEQ ID NO 11300
LENGTH: 38
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
NAME/KEY: misc feature
LOCATION: (31)..(31)
OTHER INFORMATION: n stands for inosine
US-09-371-772B-11300

Query Match 77.4%; Score 29.4; DB 4; Length 38;
Best Local Similarity 93.8%; Pred. No. 0.00034;
Matches 30; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCUGCAUUCUGAUGAGCGCCGUAUAGCGCGAANA 32
Db 1 CCUGCAUUCUGAUGAGCGCCGUAUAGCGCGAANA 32

RESULT 23
US-08-373-124A-1754
Sequence 1754, Application US/08373124A
Patent No. 5646042
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Draper, Kenneth
APPLICANT: McSwiggen, James
APPLICANT: Jarvis, Thale
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATMENT OF RESTENOSIS AND CANCER USING RIBOZYMES
TITLE OF INVENTION: CANCER USING RIBOZYMES
NUMBER OF SEQUENCES: 2627
CORRESPONDENCE ADDRESS:
ADDRESSER: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/373, 124A
FILING DATE: January 13, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/245, 466

FILING DATE: May 18, 1994
APPLICATION NUMBER: 08/192,943
FILING DATE: February 7, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/936,422
FILING DATE: August 26, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/035
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1754:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-373-124A-1754

Query Match: 76.8%; Score 29.2; DB 1; Length 38;
Best Local Similarity 91.2%; Pred. No. 0.00042;
Matches 31; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 CAUUCUGAGGCGGCUUAGCGCGAAGAAAUUCAG 38
DB 5 CAUUCUGAGGCGGCUUAGCGCGAAGAAAUUCAG 38

RESULT 24
US-08-435-628-1754
Sequence 1754, Application US/08435628
Patent No. 5817796
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Draper, Kenneth
APPLICANT: McSwiggen, James
APPLICANT: Jarvis, Thale
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TITLE OF INVENTION: TREATMENT OF RESTENOSIS AND
NUMBER OF INVENTION: CANCER USING RIBOZYMES
NUMBER OF SEQUENCES: 2627
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/435,628
FILING DATE: 05-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/373,124
FILING DATE: January 13, 1995
APPLICATION NUMBER: 08/245,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 08/192,943
FILING DATE: February 7, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/936,422

FILING DATE: August 26, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 209/035
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1754:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-435-628-1754

Query Match: 76.8%; Score 29.2; DB 1; Length 38;
Best Local Similarity 91.2%; Pred. No. 0.00042;
Matches 31; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 CAUUCUGAGGCGGCUUAGCGCGAAGAAAUUCAG 38
DB 5 CAUUCUGAGGCGGCUUAGCGCGAAGAAAUUCAG 38

RESULT 25
US-09-371-772B-8298
Sequence 8298, Application US/09371772B
Patent No. 6566127
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
APPLICANT: McSwiggen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Becbedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MBH00,876-J (237/198)
CURRENT APPLICATION NUMBER: US/09/371,772B
CURRENT FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: US 60/005,974
PRIOR FILING DATE: 1995-10-26
PRIOR APPLICATION NUMBER: US 08/584,040
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: Patentin version 3.0
SEQ ID NO 8298
LENGTH: 38
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-8298

Query Match: 76.8%; Score 29.2; DB 4; Length 38;
Best Local Similarity 91.2%; Pred. No. 0.00042;
Matches 31; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 CAUUCUGAGGCGGCUUAGCGCGAAGAAAUUCAG 38
DB 5 CAUUCUGAGGCGGCUUAGCGCGAAGAAAUUCAG 38

RESULT 26
US-09-371-772B-8707
Sequence 8707, Application US/09371772B
Patent No. 6566127
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
APPLICANT: McSwiggen, Jim
APPLICANT: Stinchcomb, Dan

APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MBH00, 876-J (237/198)
CURRENT APPLICATION NUMBER: US/09/371,772B
CURRENT FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: US 60/005,974
PRIOR FILING DATE: 1995-10-26
PRIOR APPLICATION NUMBER: US 08/584,040
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: PatentIn version 3.0
SEQ ID NO 8707
LENGTH: 38
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-8707

Query Match
Best Local Similarity 76.8%; Score 29.2; DB 4; Length 38;
Matches 31; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 GCAUUCGAGGCGGUAAGCGCGGAAAUUCAG 37
Db 4 GCAUUCGAGGCGGUAAGCGCGGAAAUUCAG 37

RESULT 27
US-09-371-772B-9621
Sequence 9621, Application US/09371772B
Patent No. 6566127
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
APPLICANT: McSwigen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MBH00, 876-J (237/198)
CURRENT APPLICATION NUMBER: US/09/371,772B
CURRENT FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: US 60/005,974
PRIOR FILING DATE: 1995-10-26
PRIOR APPLICATION NUMBER: US 08/584,040
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: PatentIn version 3.0
SEQ ID NO 9621
LENGTH: 38
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-9621

Query Match
Best Local Similarity 76.8%; Score 29.2; DB 4; Length 38;
Matches 31; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 CAUUCGAGGCGGUAAGCGCGGAAAUUCAG 38
Db 5 CAUUCGAGGCGGUAAGCGCGGAAAUUCAG 38

RESULT 28
US-09-371-772B-8786
Sequence 8786, Application US/09371772B
Patent No. 6566127
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Pavco, Pam
APPLICANT: McSwigen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MBH00, 876-J (237/198)
CURRENT APPLICATION NUMBER: US/09/371,772B
CURRENT FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: US 60/005,974
PRIOR FILING DATE: 1995-10-26
PRIOR APPLICATION NUMBER: US 08/584,040
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: PatentIn version 3.0
SEQ ID NO 8786
LENGTH: 38
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-8786

Query Match
Best Local Similarity 76.3%; Score 29; DB 4; Length 38;
Matches 32; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CCUGAUCGAGGCGGUAAGCGCGGAAAUUCAG 37
Db 1 CCUGAUCGAGGCGGUAAGCGCGGAAAUUCAG 37

RESULT 29
US-09-371-772B-10855
Sequence 10855, Application US/09371772B
Patent No. 6566127
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
APPLICANT: McSwigen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MBH00, 876-J (237/198)
CURRENT APPLICATION NUMBER: US/09/371,772B
CURRENT FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: US 60/005,974
PRIOR FILING DATE: 1995-10-26
PRIOR APPLICATION NUMBER: US 08/584,040
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: PatentIn version 3.0
SEQ ID NO 10855
LENGTH: 38
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-10855

Query Match
Best Local Similarity 76.3%; Score 29; DB 4; Length 38;
Matches 32; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CCUGAUCGAGGCGGUAAGCGCGGAAAUUCAG 37
Db 1 CCUGAUCGAGGCGGUAAGCGCGGAAAUUCAG 37

RESULT 30
US-09-371-772B-13264
Sequence 13264, Application US/09371772B

```
/ Patent No. 6566127
/ GENERAL INFORMATION:
/ APPLICANT: Ribozyme Pharmaceuticals, Inc.
/ APPLICANT: Pavco, Pam
/ APPLICANT: McSwiggen, Jim
/ APPLICANT: Stinchcomb, Dan
/ APPLICANT: Escobedo, Jaime
/ TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
/ FILE REFERENCE: MBH00,876-J (237/198)
/ CURRENT APPLICATION NUMBER: US/09/371,772B
/ PRIOR FILING DATE: 1999-08-10
/ PRIOR APPLICATION NUMBER: US 60/005,974
/ PRIOR FILING DATE: 1995-10-26
/ PRIOR APPLICATION NUMBER: US 08/584,040
/ PRIOR FILING DATE: 1996-01-08
/ NUMBER OF SEQ ID NOS: 14225
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 13264
/ LENGTH: 38
/ TYPE: RNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
/ NAME/KEY: misc_feature
/ LOCATION: (31)..(31)
/ OTHER INFORMATION: n stands for inosine
/ US-09-371-772B-13264
```

```
Query Match          76.3%; Score 29; DB 4; Length 38;
Best Local Similarity 96.7%; Pred. No. 0.00052;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 7 AUCUGAGGAGCGGUGAGCCGGAANAUA 36
Db 7 AUCUGAGGAGCGGUGAGCCGGAANAUA 36
```

```
RESULT 31
US-09-371-772B-7533
/ Sequence 7533, Application US/09371772B
/ Patent No. 6566127
/ GENERAL INFORMATION:
/ APPLICANT: Ribozyme Pharmaceuticals, Inc.
/ APPLICANT: Pavco, Pam
/ APPLICANT: McSwiggen, Jim
/ APPLICANT: Stinchcomb, Dan
/ APPLICANT: Escobedo, Jaime
/ TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
/ FILE REFERENCE: MBH00,876-J (237/198)
/ CURRENT APPLICATION NUMBER: US/09/371,772B
/ PRIOR FILING DATE: 1999-08-10
/ PRIOR APPLICATION NUMBER: US 60/005,974
/ PRIOR FILING DATE: 1995-10-26
/ PRIOR APPLICATION NUMBER: US 08/584,040
/ PRIOR FILING DATE: 1996-01-08
/ NUMBER OF SEQ ID NOS: 14225
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 7533
/ LENGTH: 38
/ TYPE: RNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
/ US-09-371-772B-7533
```

```
Query Match          75.8%; Score 28.8; DB 4; Length 38;
Best Local Similarity 93.8%; Pred. No. 0.00064;
Matches 30; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy 1 CCUGCAUCUGAGGCGGUGAGCCGGAANA 32
Db 1 CCUGCAUCUGAGGCGGUGAGCCGGAANA 32
```

```
Db 1 CUUUCANUCUGAGGCGGUGAGCCGGAANA 32
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RESULT 32
US-09-371-772B-8047
/ Sequence 8047, Application US/09371772B
/ Patent No. 6566127
/ GENERAL INFORMATION:
/ APPLICANT: Ribozyme Pharmaceuticals, Inc.
/ APPLICANT: Pavco, Pam
/ APPLICANT: McSwiggen, Jim
/ APPLICANT: Stinchcomb, Dan
/ APPLICANT: Escobedo, Jaime
/ TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
/ FILE REFERENCE: MBH00,876-J (237/198)
/ CURRENT APPLICATION NUMBER: US/09/371,772B
/ PRIOR FILING DATE: 1999-08-10
/ PRIOR APPLICATION NUMBER: US 60/005,974
/ PRIOR FILING DATE: 1995-10-26
/ PRIOR APPLICATION NUMBER: US 08/584,040
/ PRIOR FILING DATE: 1996-01-08
/ NUMBER OF SEQ ID NOS: 14225
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 8047
/ LENGTH: 38
/ TYPE: RNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
/ US-09-371-772B-8047
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Query Match          75.8%; Score 28.8; DB 4; Length 38;
Best Local Similarity 93.8%; Pred. No. 0.00064;
Matches 30; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Qy 5 CAUUCGAGGAGCGGUGAGCCGGAANAUA 36
Db 5 CAUUCGAGGAGCGGUGAGCCGGAANAUA 36
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RESULT 33
US-09-371-772B-8328
/ Sequence 8328, Application US/09371772B
/ Patent No. 6566127
/ GENERAL INFORMATION:
/ APPLICANT: Ribozyme Pharmaceuticals, Inc.
/ APPLICANT: Pavco, Pam
/ APPLICANT: McSwiggen, Jim
/ APPLICANT: Stinchcomb, Dan
/ APPLICANT: Escobedo, Jaime
/ TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
/ FILE REFERENCE: MBH00,876-J (237/198)
/ CURRENT APPLICATION NUMBER: US/09/371,772B
/ PRIOR FILING DATE: 1999-08-10
/ PRIOR APPLICATION NUMBER: US 60/005,974
/ PRIOR FILING DATE: 1995-10-26
/ PRIOR APPLICATION NUMBER: US 08/584,040
/ PRIOR FILING DATE: 1996-01-08
/ NUMBER OF SEQ ID NOS: 14225
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 8328
/ LENGTH: 38
/ TYPE: RNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
/ US-09-371-772B-8328
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Query Match          75.8%; Score 28.8; DB 4; Length 38;
Best Local Similarity 93.8%; Pred. No. 0.00064;
Matches 30; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Qy 1 CCUGAUCUGAUGAGCCGUAAGCCGAAAA 32
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Db 1 CCUAAAUCUGAUGAGCCGUAAGCCGAAAA 32

RESULT 34

US-09-371-772B-10400
; Sequence 10400, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00, 876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371, 772B
; PRIOR FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005, 974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584, 040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10400
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-10400

Query Match 75.8%; Score 28.8; DB 4; Length 38;
Best Local Similarity 93.8%; Pred. No. 0.00064;
Matches 30; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 UGCAUCUGAUGAGCCGUAAGCCGAAAAAU 34
|||
Db 3 UGCAUCUGAUGAGCCGUAAGCCGAAAAAU 34

RESULT 35

US-09-371-772B-10648
; Sequence 10648, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00, 876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371, 772B
; PRIOR FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005, 974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584, 040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10648
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-10648

Query Match 75.8%; Score 28.8; DB 4; Length 38;
Best Local Similarity 93.8%; Pred. No. 0.00064;
Matches 30; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CUGCAUCUGAUGAGCCGUAAGCCGAAAA 33
|||
Db 2 CCGAUCUGAUGAGCCGUAAGCCGAAAA 33

RESULT 36

US-09-371-772B-11044
; Sequence 11044, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00, 876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371, 772B
; PRIOR FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005, 974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584, 040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11044
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-11044

Query Match 75.8%; Score 28.8; DB 4; Length 38;
Best Local Similarity 93.8%; Pred. No. 0.00064;
Matches 30; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 MAUCUGAUGAGCCGUAAGCCGAAAAAUCAG 37
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Db 6 AUCUGAUGAGCCGUAAGCCGAAAAAUCG 37

RESULT 37

US-09-371-772B-12223
; Sequence 12223, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00, 876-J (237/198)
; CURRENT APPLICATION NUMBER: US/09/371, 772B
; PRIOR FILING DATE: 1999-08-10
; PRIOR APPLICATION NUMBER: US 60/005, 974
; PRIOR FILING DATE: 1995-10-26
; PRIOR APPLICATION NUMBER: US 08/584, 040
; PRIOR FILING DATE: 1996-01-08
; NUMBER OF SEQ ID NOS: 14225
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12223
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-371-772B-12223

OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
NAME/KEY: misc.feature
LOCATION: (31)..(31)
OTHER INFORMATION: n stands for inosine
US-09-371-772B-12223

Query Match 75.8%; Score 28.8; DB 4; Length 38;
Best Local Similarity 90.9%; Pred. No. 0.00064;
Matches 30; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 CUGCAUUCGAGAGCGCGUUGAGCCGGAANAUCAG 34
Db 2 CUGAAUUCGAGAGCGCGUUGAGCCGGAANAUC 34

RESULT 38
US-09-371-772B-12495
Sequence 12495, Application US/09371772B
Patent No. 6566127

GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam

APPLICANT: McSwiggen, Jim
APPLICANT: Escobedo, Jaime

TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor

FILE REFERENCE: MBH00,876-J (237/198)
CURRENT APPLICATION NUMBER: US/09/371,772B

PRIOR FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: US 60/005,974

PRIOR FILING DATE: 1995-10-26
PRIOR APPLICATION NUMBER: US 08/584,040

NUMBER OF SEQ ID NOS: 14225
SOFTWARE: PatentIn version 3.0

SEQ ID NO 12495
LENGTH: 38

TYPE: RNA
ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid

NAME/KEY: misc.feature
LOCATION: (31)..(31)
OTHER INFORMATION: n stands for inosine
US-09-371-772B-12495

Query Match 75.8%; Score 28.8; DB 4; Length 38;
Best Local Similarity 90.9%; Pred. No. 0.00064;
Matches 30; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 6 AAUCGAGAGCGCGUUGAGCCGGAANAUCAG 38
Db 6 AAUCGAGAGCGCGUUGAGCCGGAANAUCAG 38

RESULT 39
US-09-371-772B-13894
Sequence 13894, Application US/09371772B
Patent No. 6566127

GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam

APPLICANT: McSwiggen, Jim
APPLICANT: Stinchcomb, Dan

APPLICANT: Escobedo, Jaime

TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor

FILE REFERENCE: MBH00,876-J (237/198)
CURRENT APPLICATION NUMBER: US/09/371,772B

PRIOR FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: US 60/005,974

PRIOR FILING DATE: 1995-10-26

PRIOR APPLICATION NUMBER: US 08/584,040
PRIOR FILING DATE: 1996-01-08
NUMBER OF SEQ ID NOS: 14225
SOFTWARE: PatentIn version 3.0
SEQ ID NO 13894
LENGTH: 38

TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid

NAME/KEY: misc.feature
LOCATION: (31)..(31)
OTHER INFORMATION: n stands for inosine
US-09-371-772B-13894

Query Match 75.8%; Score 28.8; DB 4; Length 38;
Best Local Similarity 90.9%; Pred. No. 0.00064;
Matches 30; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 6 AAUCGAGAGCGCGUUGAGCCGGAANAUCAG 38
Db 6 AAUCGAGAGCGCGUUGAGCCGGAANAUCAG 38

RESULT 40
US-09-371-772B-7626
Sequence 7626, Application US/09371772B
Patent No. 6566127

GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam

APPLICANT: McSwiggen, Jim
APPLICANT: Stinchcomb, Dan

TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to Vascular Endothelial Growth Factor Receptor

FILE REFERENCE: MBH00,876-J (237/198)
CURRENT APPLICATION NUMBER: US/09/371,772B

PRIOR FILING DATE: 1999-08-10
PRIOR APPLICATION NUMBER: US 60/005,974

PRIOR FILING DATE: 1995-10-26
PRIOR APPLICATION NUMBER: US 08/584,040

NUMBER OF SEQ ID NOS: 14225
SOFTWARE: PatentIn version 3.0

SEQ ID NO 7626
LENGTH: 38

TYPE: RNA
ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid

NAME/KEY: misc.feature
LOCATION: (31)..(31)
OTHER INFORMATION: n stands for inosine
US-09-371-772B-7626

Query Match 75.3%; Score 28.6; DB 4; Length 38;
Best Local Similarity 88.6%; Pred. No. 0.0008;
Matches 31; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 UGCAUUCGAGAGCGCGUUGAGCCGGAANAUCAG 37
Db 3 UGCAUUCGAGAGCGCGUUGAGCCGGAANAUCAG 37

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Job time : 94.9636 secs

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OM nucleic - nucleic search, using bw model

Run on: May 13, 2005, 16:54:55 ; Search time 324.036 Seconds
(without alignments)
717.723 Million cell updates/sec

Title: US-09-927-046-2332

Perfect score: 38
Sequence: 1 ccugcaucugaugagcgccguuagcgcaaaaacag 38

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5662332 seqs, 3060109652 residues

Total number of hits satisfying chosen parameters: 5530346

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :

Published Applications NA:*

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- 22: /cgn2_6/ptodata/2/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	31.8	83.7	38	10	US-09-780-533A-3045
4	31.4	82.6	38	10	US-09-848-754A-4217
5	31.4	82.6	38	10	US-09-780-533A-3244
6	31.4	82.6	38	10	US-09-927-046-2304
7	31.4	82.6	38	10	US-09-877-478-3796
8	31.4	82.6	38	10	US-09-792-818-954
9	31.4	82.6	38	17	US-10-342-902-3796
10	31.4	82.6	38	18	US-10-669-841-8687
11	31.2	82.1	38	17	US-10-138-674-11175

12	31.2	82.1	38	17	US-10-138-674-11662	Sequence 11662, A
13	31.2	82.1	38	18	US-10-287-949A-11175	Sequence 11175, A
14	31.2	82.1	38	18	US-10-287-949A-11662	Sequence 11662, A
15	30.8	81.1	38	17	US-10-138-674-9749	Sequence 9749, Ap
16	30.8	81.1	38	17	US-10-138-674-10950	Sequence 10950, A
17	30.8	81.1	38	18	US-10-287-949A-9749	Sequence 9749, Ap
18	30.8	81.1	38	18	US-10-287-949A-10950	Sequence 10950, A
19	30.6	80.5	38	15	US-09-848-754A-5340	Sequence 5340, Ap
20	30.6	80.5	38	15	US-10-156-306-1007	Sequence 1007, Ap
21	30.6	80.5	38	17	US-10-138-674-11851	Sequence 11851, A
22	30.6	80.5	38	18	US-10-287-949A-11851	Sequence 11851, A
23	30.4	80.0	38	10	US-09-780-533A-3295	Sequence 3295, Ap
24	30.4	80.0	38	10	US-09-780-533A-3992	Sequence 3992, Ap
25	30.4	80.0	38	10	US-09-848-754A-4314	Sequence 4314, Ap
26	30.4	80.0	38	10	US-09-780-164-1164	Sequence 1164, Ap
27	30.4	80.0	38	17	US-10-138-674-11690	Sequence 11690, A
28	30.4	80.0	38	17	US-10-138-674-12840	Sequence 12840, A
29	30.4	80.0	38	18	US-10-287-949A-11690	Sequence 11690, A
30	30.4	80.0	38	18	US-10-287-949A-12840	Sequence 12840, A
31	30.2	79.5	38	10	US-09-780-533A-3424	Sequence 3424, Ap
32	30.2	79.5	38	17	US-10-138-674-10420	Sequence 10420, A
33	30.2	79.5	38	18	US-10-287-949A-10420	Sequence 10420, A
34	30	78.9	38	10	US-09-927-046-2660	Sequence 2660, Ap
35	30	78.9	38	10	US-09-877-478-2631	Sequence 2631, Ap
36	30	78.9	38	10	US-09-848-754A-4081	Sequence 4081, Ap
37	30	78.9	38	10	US-09-776-474-1268	Sequence 1268, Ap
38	30	78.9	38	15	US-10-156-306-814	Sequence 814, App
39	30	78.9	38	15	US-10-156-306-4583	Sequence 4583, Ap
40	30	78.9	38	17	US-10-342-902-2631	Sequence 2631, Ap
41	30	78.9	38	17	US-10-138-674-9803	Sequence 9803, Ap
42	30	78.9	38	17	US-10-138-674-10043	Sequence 10043, A
43	30	78.9	38	17	US-10-138-674-11816	Sequence 11816, A
44	30	78.9	38	18	US-10-287-949A-9803	Sequence 9803, Ap
45	30	78.9	38	18	US-10-287-949A-10043	Sequence 10043, Ap
46	30	78.9	38	18	US-10-287-949A-11816	Sequence 11816, A
47	30	78.9	38	18	US-10-669-841-7522	Sequence 7522, Ap
48	29.8	78.4	38	10	US-09-780-533A-3030	Sequence 3030, Ap
49	29.8	78.4	38	10	US-09-780-533A-3198	Sequence 3198, Ap
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51	29.8	78.4	38	10	US-09-877-478-2647	Sequence 2647, Ap
52	29.8	78.4	38	10	US-09-848-754A-5627	Sequence 5627, Ap
53	29.8	78.4	38	10	US-09-780-164-1196	Sequence 1196, Ap
54	29.8	78.4	38	15	US-10-156-306-1939	Sequence 1939, Ap
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56	29.8	78.4	38	17	US-10-138-674-10517	Sequence 10517, A
57	29.8	78.4	38	17	US-10-138-674-10622	Sequence 10622, A
58	29.8	78.4	38	17	US-10-138-674-10807	Sequence 10807, A
59	29.8	78.4	38	18	US-10-287-949A-10517	Sequence 10517, A
60	29.8	78.4	38	18	US-10-287-949A-10622	Sequence 10622, A
61	29.8	78.4	38	18	US-10-287-949A-10807	Sequence 10807, A
62	29.8	78.4	38	18	US-10-669-841-7538	Sequence 7538, Ap
63	29.6	77.9	36	9	US-09-504-231A-2430	Sequence 2430, Ap
64	29.6	77.9	36	9	US-09-274-533D-2430	Sequence 2430, Ap
65	29.6	77.9	38	9	US-09-864-785-1116	Sequence 1116, Ap
66	29.6	77.9	38	10	US-09-780-533A-3064	Sequence 3064, Ap
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68	29.6	77.9	38	10	US-09-780-533A-3951	Sequence 3951, Ap
69	29.6	77.9	38	10	US-09-927-046-2602	Sequence 2602, Ap
70	29.6	77.9	38	10	US-09-927-046-2711	Sequence 2711, Ap
71	29.6	77.9	38	10	US-09-848-754A-3972	Sequence 3972, Ap
72	29.6	77.9	38	10	US-09-848-754A-4336	Sequence 4336, Ap
73	29.6	77.9	38	10	US-09-848-754A-4999	Sequence 4999, Ap
74	29.6	77.9	38	10	US-09-776-474-1271	Sequence 1271, Ap
75	29.6	77.9	38	10	US-09-780-164-1390	Sequence 1390, Ap
76	29.6	77.9	38	15	US-10-156-306-737	Sequence 737, App
77	29.6	77.9	38	15	US-10-156-306-1112	Sequence 1112, App
78	29.6	77.9	38	15	US-10-156-306-5446	Sequence 5446, App
79	29.6	77.9	38	16	US-10-230-006-400	Sequence 400, App
80	29.6	77.9	38	17	US-10-138-674-11190	Sequence 11190, A
81	29.6	77.9	38	18	US-10-287-949A-11190	Sequence 11190, A
82	29.6	77.9	38	18	US-10-712-672-3290	Sequence 3290, App
83	29.4	77.4	38	10	US-09-780-533A-3924	Sequence 3924, App
84	29.4	77.4	38	10	US-09-927-046-2941	Sequence 2941, App

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85 29.4 77.4 38 10 US-09-877-478-2776 Sequence 2776, Ap
86 29.4 77.4 38 10 US-09-848-754A-4943 Sequence 4943, Ap
87 29.4 77.4 38 10 US-09-930-423-1858 Sequence 1858, Ap
88 29.4 77.4 38 10 US-09-745-237A-1858 Sequence 1858, Ap
89 29.4 77.4 38 15 US-10-156-306-901 Sequence 901, App
90 29.4 77.4 38 15 US-10-156-306-2009 Sequence 2009, App
91 29.4 77.4 38 17 US-10-342-902-2776 Sequence 2776, App
92 29.4 77.4 38 17 US-10-138-674-9933 Sequence 9933, App
93 29.4 77.4 38 17 US-10-138-674-10140 Sequence 10140, A
94 29.4 77.4 38 17 US-10-138-674-10699 Sequence 10699, A
95 29.4 77.4 38 17 US-10-138-674-11230 Sequence 11230, A
96 29.4 77.4 38 17 US-10-138-674-11784 Sequence 11784, A
97 29.4 77.4 38 17 US-10-138-674-11836 Sequence 11836, A
98 29.4 77.4 38 17 US-10-138-674-13577 Sequence 13577, A
99 29.4 77.4 38 18 US-10-287-949A-9933 Sequence 9933, App
100 29.4 77.4 38 18 US-10-287-949A-10140 Sequence 10140, A

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ALIGNMENTS

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RESULT 1
US-09-927-046-2332
; Sequence 2332, Application US/09927046
; Publication No. US20030064946A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc
; APPLICANT: McSwiggen, Jim
; APPLICANT: Thompson, Jim
; APPLICANT: McKenzie, Tim
; APPLICANT: Ayers, Dave
; APPLICANT: Grupe, Andrew
; APPLICANT: Szymkowski, Edmund
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chloride Channel-1
; FILE REFERENCE: 249/021
; CURRENT APPLICATION NUMBER: US/09/927,046
; CURRENT FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 5450
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2332
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-927-046-2332
Query Match 100.0%; Score 38; DB 10; Length 38;
Best Local Similarity 100.0%; Pred. No. 5.9e-07;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Q# 1 CCUGCAUCUGAUGAGGCCGUGAGCCGGAANAUCAG 38
DB 1 CCUGCAUCUGAUGAGGCCGUGAGCCGGAANAUCAG 38

RESULT 2
US-09-927-046-5432
; Sequence 5432, Application US/09927046
; Publication No. US20030064946A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc
; APPLICANT: McSwiggen, Jim
; APPLICANT: Thompson, Jim
; APPLICANT: McKenzie, Tim
; APPLICANT: Ayers, Dave
; APPLICANT: Grupe, Andrew
; APPLICANT: Szymkowski, Edmund
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chloride Channel-1
; FILE REFERENCE: 249/021
; CURRENT APPLICATION NUMBER: US/09/927,046

```

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; CURRENT FILING DATE: 2001-08-09
; NUMBER OF SEQ ID NOS: 5450
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5432
; LENGTH: 37
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; NAME/KEY: misc_feature
; LOCATION: (1)..(4)
; OTHER INFORMATION: Phosphorothioate 3'-Internucleotide Linkage
; NAME/KEY: misc_feature
; LOCATION: (1)..(8)
; OTHER INFORMATION: 2'-O-Methyl
; NAME/KEY: misc_feature
; LOCATION: (12)..(12)
; OTHER INFORMATION: 2'-O-Methyl
; NAME/KEY: misc_feature
; LOCATION: (14)..(26)
; OTHER INFORMATION: 2'-O-Methyl
; NAME/KEY: misc_feature
; LOCATION: (28)..(29)
; OTHER INFORMATION: 2'-O-Methyl
; NAME/KEY: misc_feature
; LOCATION: (31)..(36)
; OTHER INFORMATION: 2'-O-Methyl
; NAME/KEY: misc_feature
; LOCATION: (9)..(9)
; OTHER INFORMATION: 2'-deoxy-2'-C-Allyl
; NAME/KEY: misc_feature
; LOCATION: (37)..(37)
; OTHER INFORMATION: n stands for inverted deoxyabasic derivative
US-09-927-046-5432
Query Match 94.7%; Score 36; DB 10; Length 37;
Best Local Similarity 100.0%; Pred. No. 4.6e-06;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Q# 2 CCUGCAUCUGAUGAGGCCGUGAGCCGGAANAUCAG 37
DB 1 CCUGCAUCUGAUGAGGCCGUGAGCCGGAANAUCAG 36

RESULT 3
US-09-780-533A-3045
; Sequence 3045, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haeblerli, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBH00,878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3045
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-780-533A-3045
Query Match 83.7%; Score 31.8; DB 10; Length 38;
Best Local Similarity 94.3%; Pred. No. 0.00035;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

Qy 2 CUGCAUCUGAUGAGGCCGCUUAGGCCGAAAAAUAUC 36
 |||
 Db 2 CUUUAUUCUGAUGAGGCCGCUUAGGCCGAAAAAUAUC 36

RESULT 4
 US-09-848-754A-4217
 ; Sequence 4217, Application US/09848754A
 ; Publication No. US20030073207A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.
 ; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
 ; FILE REFERENCE: MBH800-958-1 (400/018)
 ; CURRENT APPLICATION NUMBER: US/09/848,754A
 ; NUMBER OF SEQ ID NOS: 9645
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 4217
 ; LENGTH: 38
 ; TYPE: RNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic acid
 US-09-848-754A-4217

Query Match 83.7%; Score 31.8; DB 10; Length 38;
 Best Local Similarity 94.3%; Pred. No. 0.00035;
 Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CUGCAUCUGAUGAGGCCGCUUAGGCCGAAAAAUAUC 36
 |||
 Db 2 CUUUAUUCUGAUGAGGCCGCUUAGGCCGAAAAAUAUC 36

RESULT 5
 US-09-780-533A-3244
 ; Sequence 3244, Application US/09780533A
 ; Publication No. US20030060611A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.
 ; APPLICANT: Blatt, Larry
 ; APPLICANT: McSwiggen, Jim
 ; APPLICANT: Chowrira, Bharat
 ; APPLICANT: Haeblerli, Pete
 ; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
 ; FILE REFERENCE: MBH800,878-A (400/011)
 ; CURRENT APPLICATION NUMBER: US/09/780,533A
 ; CURRENT FILING DATE: 2001-02-09
 ; PRIOR APPLICATION NUMBER: US 60/181,797
 ; PRIOR FILING DATE: 2000-02-11
 ; NUMBER OF SEQ ID NOS: 6679
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 3244
 ; LENGTH: 38
 ; TYPE: RNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
 US-09-780-533A-3244

Query Match 82.6%; Score 31.4; DB 10; Length 38;
 Best Local Similarity 97.0%; Pred. No. 0.00053;
 Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CAUCUGAUGAGGCCGCUUAGGCCGAAAAAUAUC 37
 |||
 Db 5 CAUCUGAUGAGGCCGCUUAGGCCGAAAAAUAUC 37

RESULT 6
 US-09-927-046-2304

; Sequence 2304, Application US/09927046
 ; Publication No. US20030064946A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc
 ; APPLICANT: McSwiggen, Jim
 ; APPLICANT: Thompson, Jim
 ; APPLICANT: McKenzie, Tim
 ; APPLICANT: Ayers, Dave
 ; APPLICANT: Grube, Andrew
 ; APPLICANT: Szymkowski, Edmund
 ; TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chloric
 ; FILE REFERENCE: 249/021
 ; CURRENT APPLICATION NUMBER: US/09/927,046
 ; CURRENT FILING DATE: 2001-08-09
 ; NUMBER OF SEQ ID NOS: 5450
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 2304
 ; LENGTH: 38
 ; TYPE: RNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
 US-09-927-046-2304

Query Match 82.6%; Score 31.4; DB 10; Length 38;
 Best Local Similarity 97.0%; Pred. No. 0.00053;
 Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 UGAAUUCUGAUGAGGCCGCUUAGGCCGAAAAAUAUC 35
 |||
 Db 3 UGAAUUCUGAUGAGGCCGCUUAGGCCGAAAAAUAUC 35

RESULT 7
 US-09-877-478-3796
 ; Sequence 3796, Application US/09877478
 ; Publication No. US20030068301A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ribozyme Pharmaceuticals, Inc.
 ; APPLICANT: Draper, Kenneth
 ; APPLICANT: Blatt, Larry
 ; APPLICANT: McSwiggen, Jim
 ; APPLICANT: Morrissey, Jaim
 ; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
 ; FILE REFERENCE: MBH800-845-H (400/029)
 ; CURRENT APPLICATION NUMBER: US/09/877,478
 ; CURRENT FILING DATE: 2001-12-31
 ; PRIOR APPLICATION NUMBER: US 07/882,712
 ; PRIOR FILING DATE: 1992-05-14
 ; PRIOR APPLICATION NUMBER: US 09/531,025
 ; PRIOR FILING DATE: 2000-03-20
 ; PRIOR APPLICATION NUMBER: US 09/636,385
 ; PRIOR FILING DATE: 2000-08-09
 ; PRIOR APPLICATION NUMBER: US 09/696,347
 ; PRIOR FILING DATE: 2000-10-24
 ; PRIOR APPLICATION NUMBER: US 08/193,627
 ; PRIOR FILING DATE: 1994-02-07
 ; PRIOR APPLICATION NUMBER: US 08/433,993
 ; PRIOR FILING DATE: 1995-05-04
 ; PRIOR APPLICATION NUMBER: US 08/434,504
 ; PRIOR FILING DATE: 1995-05-04
 ; PRIOR APPLICATION NUMBER: US 09/436,430
 ; PRIOR FILING DATE: 1999-11-08
 ; NUMBER OF SEQ ID NOS: 6586
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 3796
 ; LENGTH: 38
 ; TYPE: RNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
 ; NAME/KEY: misc_feature

LOCATION: (31)..(31)
OTHER INFORMATION: n stands for inosine
US-09-877-478-3796

Query Match
Best Local Similarity 82.6%; Score 31.4; DB 10; Length 38;
Matches 32; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCUGCAUCUGAUGAGCGCGUAGGCCGAAAAAU 34
Db 1 CCUGCAACUGAUGAGCGCGUAGGCCGAAAAAU 34

RESULT 8
US-09-792-818-954

Sequence 954, Application US/09792818
Publication No. US20030134806A1

GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.

APPLICANT: Jarvis, Thale
APPLICANT: Von Carlowitz, Ira

APPLICANT: McSwiggen, Jim
APPLICANT: Hamblin, Paul

APPLICANT: Ellis, Jonathan
TITLE OF INVENTION: Method and Reagent for the Inhibition of Grb-2-related with Inse

FILE REFERENCE: MBH00-901-A (400/013)
CURRENT APPLICATION NUMBER: US/09/792,818

CURRENT FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 2304

SOFTWARE: PatentIn version 3.0
SEQ ID NO 954

LENGTH: 38
TYPE: RNA

ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-792-818-954

Query Match
Best Local Similarity 82.6%; Score 31.4; DB 10; Length 38;
Matches 32; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GCAUUCGUAUGAGCGCGUAGGCCGAAAAAUCA 36
Db 4 GCAUCUGAUGAGCGCGUAGGCCGAAAAAUCA 36

RESULT 9
US-10-342-902-3796

Sequence 3796, Application US/10342902
Publication No. US20040054156A1

GENERAL INFORMATION:
APPLICANT: Sirna Therapeutics, Inc.

APPLICANT: Draper, Kenneth
APPLICANT: Blact, Larry

APPLICANT: McSwiggen, Jim
APPLICANT: Morrissey, Dave

TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
FILE REFERENCE: 400/075 (MBH00-845-I)

CURRENT APPLICATION NUMBER: US/10/342,902
CURRENT FILING DATE: 2003-01-15

PRIOR APPLICATION NUMBER: US 09/877,478
PRIOR FILING DATE: 2001-06-08

PRIOR APPLICATION NUMBER: US 09/531,025
PRIOR FILING DATE: 2000-03-20

PRIOR APPLICATION NUMBER: US 09/636,385
PRIOR FILING DATE: 2000-08-09

PRIOR APPLICATION NUMBER: US 09/696,347
PRIOR FILING DATE: 2000-10-24

PRIOR APPLICATION NUMBER: US 08/193,627
PRIOR FILING DATE: 1994-02-07

PRIOR APPLICATION NUMBER: US 07/882,712

PRIOR FILING DATE: 1992-05-14
PRIOR APPLICATION NUMBER: US 09/436,430
PRIOR FILING DATE: 1992-11-08

NUMBER OF SEQ ID NOS: 6592
SOFTWARE: PatentIn version 3.2

SEQ ID NO 3796
LENGTH: 38

TYPE: RNA
ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid

NAME/KEY: misc_feature
LOCATION: (31)..(31)

OTHER INFORMATION: n stands for inosine
US-10-342-902-3796

Query Match
Best Local Similarity 82.6%; Score 31.4; DB 17; Length 38;
Matches 32; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCUGCAUCUGAUGAGCGCGUAGGCCGAAAAAU 34
Db 1 CCUGCAACUGAUGAGCGCGUAGGCCGAAAAAU 34

RESULT 10
US-10-669-841-8687

Sequence 8687, Application US/10669841
Publication No. US20040127446A1

GENERAL INFORMATION:
APPLICANT: Sirna Therapeutics, Inc.

APPLICANT: Lawrence, Blact
APPLICANT: Dennis, Macejak

APPLICANT: James, McSwiggen
APPLICANT: Pamela, Pavco

APPLICANT: David, Morrissey
APPLICANT: Patricia, Lee

APPLICANT: Kenneth, Draper
APPLICANT: Elisabeth, Roberts

TITLE OF INVENTION: Oligonucleotide Mediated Inhibition of Hepatitis B Virus and HEPN
TITLE OF INVENTION: VIRUS REPLICATION

FILE REFERENCE: 400/042US (MBH02-249-E)
CURRENT APPLICATION NUMBER: US/10/669,841

CURRENT FILING DATE: 2003-09-23
PRIOR APPLICATION NUMBER: PCT/US02/09187

PRIOR FILING DATE: 2002-03-26
PRIOR APPLICATION NUMBER: US 60/296,876

PRIOR FILING DATE: 2001-06-08
PRIOR APPLICATION NUMBER: US 60/335,059

PRIOR FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: US 60/337,055

PRIOR FILING DATE: 2001-12-05
PRIOR APPLICATION NUMBER: US 60/358,580

PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/363,124

PRIOR FILING DATE: 2002-03-11
PRIOR APPLICATION NUMBER: US 09/817,879

PRIOR FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: US 09/740,332

PRIOR FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: US 09/611,931

PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: US 09/504,321

PRIOR FILING DATE: 2000-02-15
Remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 16207
SOFTWARE: PatentIn version 3.0

SEQ ID NO 8687
LENGTH: 38

TYPE: RNA
ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
FEATURE:
NAME/KEY: misc feature
LOCATION: (31)..(31)
OTHER INFORMATION: n stands for inosine
US-10-669-841-8687

Query Match 82.6%; Score 31.4; DB 18; Length 38;
Best Local Similarity 94.1%; Pred. No. 0.00053;
Matches 32; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCUGCAUUCGUAUGAGCGCCGUAAGCCGAAAUU 34
DB 1 CCUGCAUUCGUAUGAGCGCCGUAAGCCGAAAUU 34

RESULT 11
US-10-138-674-11175
Sequence 11175, Application US/10138674
Publication No. US2004007565A1
GENERAL INFORMATION:
APPLICANT: Ribozyne Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
APPLICANT: MCSwigen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MBH00-876-N (400/049)
CURRENT APPLICATION NUMBER: US/10/138,674
CURRENT FILING DATE: 2002-05-03
NUMBER OF SEQ ID NOS: 20822
SOFTWARE: PatentIn version 3.0
SEQ ID NO 11175
LENGTH: 38
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-138-674-11175

Query Match 82.1%; Score 31.2; DB 17; Length 38;
Best Local Similarity 91.7%; Pred. No. 0.00065;
Matches 33; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCUGCAUUCGUAUGAGCGCCGUAAGCCGAAAUU 36
DB 1 CCUGCAUUCGUAUGAGCGCCGUAAGCCGAAAUU 36

RESULT 12
US-10-138-674-11662
Sequence 11662, Application US/10138674
Publication No. US2004007565A1
GENERAL INFORMATION:
APPLICANT: Ribozyne Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
APPLICANT: MCSwigen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MBH00-876-N (400/049)
CURRENT APPLICATION NUMBER: US/10/138,674
CURRENT FILING DATE: 2002-05-03
NUMBER OF SEQ ID NOS: 20822
SOFTWARE: PatentIn version 3.0
SEQ ID NO 11662
LENGTH: 38
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid

US-10-138-674-11662

Query Match 82.1%; Score 31.2; DB 17; Length 38;
Best Local Similarity 91.7%; Pred. No. 0.00065;
Matches 33; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCUGCAUUCGUAUGAGCGCCGUAAGCCGAAAUU 36
DB 1 CCUGCAUUCGUAUGAGCGCCGUAAGCCGAAAUU 36

RESULT 13
US-10-287-949A-11175
Sequence 11175, Application US/10287949A
Publication No. US20040102389A1
GENERAL INFORMATION:
APPLICANT: Ribozyne Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
APPLICANT: MCSwigen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MBH00-876-N (400/049)
CURRENT APPLICATION NUMBER: US/10/287,949A
CURRENT FILING DATE: 2003-04-11
NUMBER OF SEQ ID NOS: 20822
SOFTWARE: PatentIn version 3.0
SEQ ID NO 11175
LENGTH: 38
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-287-949A-11175

Query Match 82.1%; Score 31.2; DB 18; Length 38;
Best Local Similarity 91.7%; Pred. No. 0.00065;
Matches 33; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCUGCAUUCGUAUGAGCGCCGUAAGCCGAAAUU 36
DB 1 CCUGCAUUCGUAUGAGCGCCGUAAGCCGAAAUU 36

RESULT 14
US-10-287-949A-11662
Sequence 11662, Application US/10287949A
Publication No. US20040102389A1
GENERAL INFORMATION:
APPLICANT: Ribozyne Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
APPLICANT: MCSwigen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MBH00-876-N (400/049)
CURRENT APPLICATION NUMBER: US/10/287,949A
CURRENT FILING DATE: 2003-04-11
NUMBER OF SEQ ID NOS: 20822
SOFTWARE: PatentIn version 3.0
SEQ ID NO 11662
LENGTH: 38
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-287-949A-11662

Query Match 82.1%; Score 31.2; DB 18; Length 38;
Best Local Similarity 91.7%; Pred. No. 0.00065;
Matches 33; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 CCUGCAUCUGAUGAGCGCGUUGAGCCGAAAAAUC 36
DB 1 CCGCAAGCUGAUGAGCGCGUUGAGCCGAAAAAUC 36

RESULT 15

US-10-138-674-9749
; Sequence 9749, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Relating to Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9749
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-138-674-9749

Query Match 81.1%; Score 30.8; DB 17; Length 38;
Best Local Similarity 94.1%; Pred. No. 0.00098;
Matches 32; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 CUGCAUCUGAUGAGCGCGUUGAGCCGAAAAAUC 35
DB 2 CCGCAAGCUGAUGAGCGCGUUGAGCCGAAAAAUC 35

RESULT 16
US-10-138-674-10950
; Sequence 10950, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Relating to Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10950
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-138-674-10950

Query Match 81.1%; Score 30.8; DB 17; Length 38;
Best Local Similarity 94.1%; Pred. No. 0.00098;
Matches 32; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CCUGCAUCUGAUGAGCGCGUUGAGCCGAAAAAUC 34
DB 1 CCUGCAAGCUGAUGAGCGCGUUGAGCCGAAAAAUC 34

RESULT 17
US-10-287-949A-9749
; Sequence 9749, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Relating to Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9749
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-287-949A-9749

Query Match 81.1%; Score 30.8; DB 18; Length 38;
Best Local Similarity 94.1%; Pred. No. 0.00098;
Matches 32; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 2 CUGCAUCUGAUGAGCGCGUUGAGCCGAAAAAUC 35
DB 2 CCGCAAGCUGAUGAGCGCGUUGAGCCGAAAAAUC 35

RESULT 18
US-10-287-949A-10950
; Sequence 10950, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Relating to Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBH00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10950
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-287-949A-10950

Query Match 81.1%; Score 30.8; DB 18; Length 38;
Best Local Similarity 94.1%; Pred. No. 0.00098;
Matches 32; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 CCUGCAUCUGAUGAGCGCGUUGAGCCGAAAAAUC 34
DB 1 CCUGCAAGCUGAUGAGCGCGUUGAGCCGAAAAAUC 34

RESULT 19
US-09-848-754A-5340
; Sequence 5340, Application US/09848754A
; Publication No. US20030073207A1

GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to
TITLE OF INVENTION: Levels of Bifidobacterial Growth Factor Receptors
FILE REFERENCE: MBH00-958-1 (400/018)
CURRENT APPLICATION NUMBER: US/09/848,754A
CURRENT FILING DATE: 2001-05-03
NUMBER OF SEQ ID NOS: 9645
SOFTWARE: PatentIn version 3.0
SEQ ID NO 5340
LENGTH: 38
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic acid
NAME/KEY: misc_feature
LOCATION: (31)..(31)
OTHER INFORMATION: n stands for inosine
US-09-848-754A-5340

Query Match 80.5%; Score 30.6; DB 10; Length 38;
Best Local Similarity 86.8%; Pred. No. 0.0012;
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CCUGCAUCUGAUGAGCGCCGUAAGCGCGGAAAAAUCAGG 38
Db 1 CCUGCAUCUGAUGAGCGCCGUAAGCGCGGAAAAAUCAGG 38

RESULT 20
US-10-156-306-1007
Sequence 1007, Application US/10156306
Publication No. US20030119017A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: McSwiggen, James
TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related to
TITLE OF INVENTION: Levels of IKK-gamma and PKR
FILE REFERENCE: MBH01-664-A (400/050)
CURRENT APPLICATION NUMBER: US/10/156,306
CURRENT FILING DATE: 2002-05-28
NUMBER OF SEQ ID NOS: 8013
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1007
LENGTH: 38
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-156-306-1007

Query Match 80.5%; Score 30.6; DB 15; Length 38;
Best Local Similarity 89.2%; Pred. No. 0.0012;
Matches 33; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CCUGCAUCUGAUGAGCGCCGUAAGCGCGGAAAAAUCAGG 37
Db 1 CCUGCAUCUGAUGAGCGCCGUAAGCGCGGAAAAAUCAGG 37

RESULT 21
US-10-138-674-11851
Sequence 11851, Application US/10138674
Publication No. US20040077565A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
APPLICANT: McSwiggen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MBH00-876-N (400/049)

CURRENT APPLICATION NUMBER: US/10/138,674
CURRENT FILING DATE: 2002-05-03
NUMBER OF SEQ ID NOS: 20822
SOFTWARE: PatentIn version 3.0
SEQ ID NO 11851
LENGTH: 38
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-138-674-11851

Query Match 80.5%; Score 30.6; DB 17; Length 38;
Best Local Similarity 89.2%; Pred. No. 0.0012;
Matches 33; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 CUCCAUUCUGAUGAGCGCCGUAAGCGCGGAAAAAUCAGG 38
Db 2 CUCCAUUCUGAUGAGCGCCGUAAGCGCGGAAAAAUCAGG 38

RESULT 22
US-10-287-949A-11851
Sequence 11851, Application US/10287949A
Publication No. US20040102389A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
APPLICANT: McSwiggen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Related to
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
FILE REFERENCE: MBH00-876-N (400/049)
CURRENT APPLICATION NUMBER: US/10/287,949A
CURRENT FILING DATE: 2003-04-11
NUMBER OF SEQ ID NOS: 20822
SOFTWARE: PatentIn version 3.0
SEQ ID NO 11851
LENGTH: 38
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-287-949A-11851

Query Match 80.5%; Score 30.6; DB 18; Length 38;
Best Local Similarity 89.2%; Pred. No. 0.0012;
Matches 33; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 CUCCAUUCUGAUGAGCGCCGUAAGCGCGGAAAAAUCAGG 38
Db 2 CUCCAUUCUGAUGAGCGCCGUAAGCGCGGAAAAAUCAGG 38

RESULT 23
US-09-780-533A-3295
Sequence 3295, Application US/09780533A
Publication No. US20030060611A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Blact, Larry
APPLICANT: McSwiggen, Jim
APPLICANT: Chowhira, Bharat
APPLICANT: Haebertl, Pete
TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
FILE REFERENCE: MBH00,878-A (400/011)
CURRENT APPLICATION NUMBER: US/09/780,533A
CURRENT FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: US 60/181,797
PRIOR FILING DATE: 2000-02-11
NUMBER OF SEQ ID NOS: 6679
SOFTWARE: PatentIn version 3.0

```
; SEQ ID NO 3295
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-780-533A-3295

Query Match
Best Local Similarity 80.0%; Score 30.4; DB 10; Length 38;
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CAUCUGAUGAGCGCCGUAAGCGCGAANAUA 36
DB 5 CAACUGAUGAGCGCCGUAAGCGCGAANAUA 36

RESULT 24
US-09-780-533A-3992
; Sequence 3992, Application US/09780533A
; Publication No. US20030060611A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; APPLICANT: Chowrita, Bharat
; APPLICANT: Haeblerl, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MBHB00, 878-A (400/011)
; CURRENT APPLICATION NUMBER: US/09/780,533A
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3992
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
; NAME/KEY: misc_feature
; LOCATION: (31)..(31)
; OTHER INFORMATION: n stands for inosine
US-09-780-533A-3992

Query Match
Best Local Similarity 80.0%; Score 30.4; DB 10; Length 38;
Matches 31; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CUGCAUUCUGAUGAGCGCCGUAAGCGCGAANAUA 34
DB 2 CUGCAUUCUGAUGAGCGCCGUAAGCGCGAANAUA 34

RESULT 25
US-09-848-754A-4314
; Sequence 4314, Application US/09848754A
; Publication No. US20030073207A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
; FILE REFERENCE: MBHB00-958-I (400/018)
; CURRENT APPLICATION NUMBER: US/09/848,754A
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 9645
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4314
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
```

```
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic acid
US-09-848-754A-4314

Query Match
Best Local Similarity 80.0%; Score 30.4; DB 10; Length 38;
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 AUCUGAUGAGCGCCGUAAGCGCGAANAUCAG 38
DB 7 AUCUGAUGAGCGCCGUAAGCGCGAANAUCAG 38

RESULT 26
US-09-780-164-1164
; Sequence 1164, Application US/09780164
; Publication No. US20030092646A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: McSwiggen, Jim
; TITLE OF INVENTION: Method and Reagent for the Inhibition of CD20
; FILE REFERENCE: 400/010
; CURRENT APPLICATION NUMBER: US/09/780,164
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/185,516
; NUMBER OF SEQ ID NOS: 2603
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1164
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-780-164-1164

Query Match
Best Local Similarity 80.0%; Score 30.4; DB 10; Length 38;
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CAUCUGAUGAGCGCCGUAAGCGCGAANAUA 36
DB 5 CAUCUGAUGAGCGCCGUAAGCGCGAANAUA 36

RESULT 27
US-10-138-674-11690
; Sequence 11690, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; PRIOR FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11690
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-138-674-11690

Query Match
Best Local Similarity 80.0%; Score 30.4; DB 17; Length 38;
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

QY 1 CCUGCAUUCUGAGCGCCGUUAGCGCGAATA 32
DB 1 CCUGCAAGCUGAGCGCCGUUAGCGCGAATA 32

RESULT 28
US-10-138-674-12840
; Sequence 12840, Application US/10138674
; Publication No. US2004007565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: MCSwigen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Relating to the Growth of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MHB00-876-N (400/049)
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12840
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-138-674-12840

Query Match
Best Local Similarity 96.9%; Score 30.4; DB 17; Length 38;
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 AUCUGAGAGCGCCGUUAGCGCGAATAAUCAGG 38
DB 7 AGCUGAGAGCGCCGUUAGCGCGAATAAUCAGG 38

RESULT 29
US-10-287-949A-11690
; Sequence 11690, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: MCSwigen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Relating to the Growth of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MHB00-876-N (400/049)
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11690
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-287-949A-11690

Query Match
Best Local Similarity 96.9%; Score 30.4; DB 18; Length 38;
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCUGCAUUCUGAGCGCCGUUAGCGCGAATA 32
DB 1 CCUGCAAGCUGAGCGCCGUUAGCGCGAATA 32

RESULT 30
US-10-287-949A-12840
; Sequence 12840, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: MCSwigen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Relating to the Growth of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MHB00-876-N (400/049)
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12840
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-287-949A-12840

US-10-287-949A-12840

Query Match
Best Local Similarity 96.9%; Score 30.4; DB 18; Length 38;
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 AUCUGAGAGCGCCGUUAGCGCGAATAAUCAGG 38
DB 7 AGCUGAGAGCGCCGUUAGCGCGAATAAUCAGG 38

RESULT 31
US-09-780-533A-3424
; Sequence 3424, Application US/09780533A
; Publication No. US2003006061A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Blatt, Larry
; APPLICANT: MCSwigen, Jim
; APPLICANT: Chowrira, Bharat
; APPLICANT: Haeblerl, Pete
; TITLE OF INVENTION: Method and Reagent for the Inhibition of NOGO Gene
; FILE REFERENCE: MHB00-876-A (400/011)
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/181,797
; PRIOR FILING DATE: 2000-02-11
; NUMBER OF SEQ ID NOS: 6679
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3424
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-780-533A-3424

Query Match
Best Local Similarity 91.4%; Score 30.2; DB 10; Length 38;
Matches 32; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CCUGCAUUCUGAGCGCCGUUAGCGCGAATAAUC 36
DB 2 CUGCAACUGAGAGCGCCGUUAGCGCGAATAAUC 36

RESULT 32
US-10-138-674-10420
; Sequence 10420, Application US/10138674

```
Publication No. US20040077565A1
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
APPLICANT: McSwiggen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
FILE REFERENCE: MBH00-876-N (400/049)
CURRENT FILING DATE: 2002-05-03
NUMBER OF SEQ ID NOS: 20822
SOFTWARE: PatentIn version 3.0
SEQ ID NO 10420
LENGTH: 38
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-138-674-10420
```

```
Query Match
Best Local Similarity 79.5%; Score 30.2; DB 17; Length 38;
Matches 32; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 2 CUGCAUUCUGAUGAGCCGCUUAGCCGGAUUAUCA 36
DB 2 CUACAGUCUGAUGAGCCGCUUAGCCGGAUUAUCA 36
```

```
RESULT 33
US-10-287-949A-10420
Sequence 10420, Application US/10287949A
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Pavco, Pam
APPLICANT: McSwiggen, Jim
APPLICANT: Stinchcomb, Dan
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
FILE REFERENCE: MBH00-876-N (400/049)
CURRENT FILING DATE: 2003-04-11
NUMBER OF SEQ ID NOS: 20822
SOFTWARE: PatentIn version 3.0
SEQ ID NO 10420
LENGTH: 38
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-287-949A-10420
```

```
Query Match
Best Local Similarity 79.5%; Score 30.2; DB 18; Length 38;
Matches 32; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 2 CUGCAUUCUGAUGAGCCGCUUAGCCGGAUUAUCA 36
DB 2 CUACAGUCUGAUGAGCCGCUUAGCCGGAUUAUCA 36
```

```
RESULT 34
US-09-927-046-2660
Sequence 2660, Application US/099277046
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc
APPLICANT: McSwiggen, Jim
APPLICANT: Thompson, Jim
```

```
APPLICANT: McKenzie, Tim
APPLICANT: Ayers, Dave
APPLICANT: Grube, Andrew
APPLICANT: Szymkowski, Edmund
TITLE OF INVENTION: Method and Reagent for the Inhibition of Calcium Activated Chloric
FILE REFERENCE: 249/021
CURRENT APPLICATION NUMBER: US/09/927,046
CURRENT FILING DATE: 2001-08-09
NUMBER OF SEQ ID NOS: 5450
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2660
LENGTH: 38
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-927-046-2660
```

```
Query Match
Best Local Similarity 78.9%; Score 30; DB 10; Length 38;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 4 GCNAUCUGAUGAGCCGCUUAGCCGGAUUA 33
DB 4 GCNAUCUGAUGAGCCGCUUAGCCGGAUUA 33
```

```
RESULT 35
US-09-877-478-2631
Sequence 2631, Application US/09877478
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
APPLICANT: Draper, Kenneth
APPLICANT: Blatt, Larry
APPLICANT: McSwiggen, Jim
APPLICANT: Morrissey, Dave
TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
FILE REFERENCE: MBH00-845-H (400/029)
CURRENT FILING DATE: US/09/877,478
PRIOR APPLICATION NUMBER: US 07/882,712
PRIOR FILING DATE: 1992-05-14
PRIOR APPLICATION NUMBER: US 09/531,025
PRIOR FILING DATE: 2000-03-20
PRIOR APPLICATION NUMBER: US 09/636,385
PRIOR FILING DATE: 2000-08-09
PRIOR APPLICATION NUMBER: US 09/696,347
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 08/193,627
PRIOR FILING DATE: 1994-02-07
PRIOR APPLICATION NUMBER: US 08/433,993
PRIOR FILING DATE: 1995-05-04
PRIOR APPLICATION NUMBER: US 08/434,504
PRIOR FILING DATE: 1995-05-04
PRIOR APPLICATION NUMBER: US 09/436,430
PRIOR FILING DATE: 1999-11-08
NUMBER OF SEQ ID NOS: 6586
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2631
LENGTH: 38
TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-09-877-478-2631
```

```
Query Match
Best Local Similarity 78.9%; Score 30; DB 10; Length 38;
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```
QY 1 CCUGCAUUCUGAUGAGCCGCUUAGCCGGAUUAUCA 38
```

Db 1 CCACAGCUGAUGAGCCGUAAGCCGAAAGUAGG 38

RESULT 36
US-09-848-754A-4081
; Sequence 4081, Application US/09848754A
; Publication No. US20030073207A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; TITLE OF INVENTION: Levels of Epidermal Growth Factor Receptors
; FILE REFERENCE: MBH00-958-1 (400/018)
; CURRENT APPLICATION NUMBER: US/09/848,754A
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 9645
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4081
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic acid
US-09-848-754A-4081

Query Match 78.9%; Score 30; DB 10; Length 38;
Best Local Similarity 86.8%; Pred. No. 0.0022;
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CCUGCAUCUGAUGAGCCGUAAGCCGAAAUAGG 38
Db 1 CCUGCAUCUGAUGAGCCGUAAGCCGAAAUAGG 38

RESULT 37
US-09-776-474-1268
; Sequence 1268, Application US/09776474
; Publication No. US20030087847A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: Jarvis, Thale
; APPLICANT: Bochner, Robert
; APPLICANT: Holman, Patricia
; APPLICANT: Fattaey, Ali
; APPLICANT: McSwigen, Jim
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Checkpoint Kinase-1 (CHK
; TITLE OF INVENTION: Enzyme
; FILE REFERENCE: MBH00-955-A (400/008)
; CURRENT APPLICATION NUMBER: US/09/776,474
; CURRENT FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: US 60/179,983
; PRIOR FILING DATE: 2000-03-02
; NUMBER OF SEQ ID NOS: 2992
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1268
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid
US-09-776-474-1268

Query Match 78.9%; Score 30; DB 10; Length 38;
Best Local Similarity 86.8%; Pred. No. 0.0022;
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CCUGCAUCUGAUGAGCCGUAAGCCGAAAUAGG 38
Db 1 CCUGCAUCUGAUGAGCCGUAAGCCGAAAUAGG 38

RESULT 38
US-10-156-306-814

; Sequence 814, Application US/10156306
; Publication No. US20030119017A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: McSwigen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; TITLE OF INVENTION: Levels of IKK-gamma and PKR
; FILE REFERENCE: MBH01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/10/156,306
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8013
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 814
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-156-306-814

Query Match 78.9%; Score 30; DB 15; Length 38;
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 AAUCUGAUGAGCCGUAAGCCGAAAUAGG 35
Db 6 AAUCUGAUGAGCCGUAAGCCGAAAUAGG 35

RESULT 39
US-10-156-306-4583
; Sequence 4583, Application US/10156306
; Publication No. US20030119017A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyne Pharmaceuticals, Inc.
; APPLICANT: McSwigen, James
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Related
; TITLE OF INVENTION: Levels of IKK-gamma and PKR
; FILE REFERENCE: MBH01-664-A (400/050)
; CURRENT APPLICATION NUMBER: US/10/156,306
; CURRENT FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 8013
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4583
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-156-306-4583

Query Match 78.9%; Score 30; DB 15; Length 38;
Best Local Similarity 86.8%; Pred. No. 0.0022;
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CCUGCAUCUGAUGAGCCGUAAGCCGAAAUAGG 38
Db 1 CCUGCAUCUGAUGAGCCGUAAGCCGAAAUAGG 38

RESULT 40
US-10-342-902-2631
; Sequence 2631, Application US/10342902
; Publication No. US20040054156A1
; GENERAL INFORMATION:
; APPLICANT: Sina Therapeutics, Inc.
; APPLICANT: Draper, Kenneth
; APPLICANT: Blatt, Larry
; APPLICANT: McSwigen, Jim
; APPLICANT: Morrissey, Dave
; TITLE OF INVENTION: Method and Reagent for Inhibiting Hepatitis B Virus Replication
; FILE REFERENCE: 400/075 (MBH00-845-1)
; CURRENT APPLICATION NUMBER: US/10/342,902

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; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 09/877,478
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 09/531,025
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 09/636,385
; PRIOR FILING DATE: 2000-08-09
; PRIOR APPLICATION NUMBER: US 09/696,347
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 08/193,627
; PRIOR FILING DATE: 1994-02-07
; PRIOR APPLICATION NUMBER: US 07/882,712
; PRIOR FILING DATE: 1992-05-14
; PRIOR APPLICATION NUMBER: US 09/436,430
; NUMBER OF SEQ ID NOS: 6592
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 2631
; LENGTH: 38
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
US-10-342-902-2631

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Query Match      78.9%; Score 30; DB 17; Length 38;
Best Local Similarity 86.8%; Pred. No. 0.0022;
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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QY      1 CCUGCAUUCGUAUGAGGCCGUAAGCGCAAAAUAUCAGG 38
Db      1 CCACGAGCUGAUGAGGCCGUAAGCGCAAAAUAUCAGG 38

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Search completed: May 13, 2005, 18:25:02
Job time : 326.036 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 13, 2005, 16:42:23 ; Search time 1848.87 Seconds
(without alignments)
782.337 Million cell updates/sec

Title: US-09-927-046-2332

Perfect score: 38
Sequence: 1 ccgcaucugaugagcgccguuagcgcaaaaucagc 38

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 675282

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :
EST:*
1: gb_esc1:*
2: gb_esc2:*
3: gb_hic:*
4: gb_esc3:*
5: gb_esc4:*
6: gb_esc5:*
7: gb_esc6:*
8: gb_gsa1:*
9: gb_gsa2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	17.6	46.3	63 1	AI313954 u149601.Y
2	17.2	45.3	59 8	AZ368574 1M0118A16
3	17	44.7	70 1	AA666597 vm49401.r
4	17	44.7	84 9	AL765388 Arabidops
5	17	44.7	92 8	BH803188 1008099D0
6	17	44.7	94 8	AZ807494 2M0070F19
7	16.8	44.2	50 1	AU105965 AU105965
8	16.8	44.2	50 1	AU105967 AU105967
9	16.8	44.2	55 1	AI341480 qg94b11.x
10	16.6	43.7	91 1	AV367851 AV367851
11	16.4	43.2	67 9	BX655236 Arabidops
12	16.4	43.2	100 7	CN165896 996741.MA
13	16.2	42.6	90 8	BH913847 3526.1.41
14	16.2	42.1	73 6	CD971713 ONE17h01
15	16	42.1	82 9	AJ597197 Arabidops
16	16	42.1	91 4	BU029544 BU029544
17	16	42.1	94 1	AI204769 ZF-EST88
18	16	42.1	97 1	AA237314 mx17b12.r
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20	15.8	41.6	69 6	CA567380 Arabidops
21	15.8	41.6	72 6	CD963815 SPY_106_G
22	15.8	41.6	76 6	CA796314 CgC_BL_33
23	15.8	41.6	89 4	BG062646 LG955G10-
24	15.8	41.6	92 9	CG663893 OST450022

C 25	15.8	41.6	94 6	CD947628 SAA_70_Ge
C 26	15.8	41.6	94 7	CV519527 Arabidops
C 27	15.8	41.6	94 9	CG528153 OST1071142
C 28	15.8	41.6	97 8	AZ608536 1M0432N13
C 29	15.8	41.6	98 8	AZ481971 1M0306J08
C 30	15.8	41.6	98 8	AZ566002 215PVB01
C 31	15.6	41.1	41 9	AJ590916 Arabidops
C 32	15.6	41.1	76 1	AI702572 w680D03.x
C 33	15.6	41.1	76 7	w72704 zdt7c05.81
C 34	15.6	41.1	78 9	CG547582 OST148394
C 35	15.6	41.1	80 9	CG545569 OST143941
C 36	15.6	41.1	90 1	AA286563 v084e07.r
C 37	15.6	41.1	97 1	AI1318202 t552a03.x
C 38	15.6	41.1	99 4	BG881971 eae92c02.
C 39	15.6	41.1	100 7	CV316867 CM2-BN018
C 40	15.4	40.5	51 9	CC483070 CH240.311
C 41	15.4	40.5	56 9	BX286908 Arabidops
C 42	15.4	40.5	77 6	CD531375 10110_Ara
C 43	15.4	40.5	79 1	AA889445 A381h12.8
C 44	15.4	40.5	80 8	AZ502082 1M0341N09
C 45	15.4	40.5	82 4	BG673231 DRNB007
C 46	15.4	40.5	84 1	AL666581 AL666581
C 47	15.4	40.5	85 7	CF916999 Bf10r498.
C 48	15.4	40.5	87 7	CN920518 000511A8A
C 49	15.4	40.5	88 1	AA474045 v654D03.r
C 50	15.4	40.5	92 5	BG655365 1112119E0
C 51	15.4	40.5	100 7	CF317848 HD--07-L0
C 52	15.4	40.5	100 9	BX002767 Arabidops
C 53	15.2	40.0	48 8	AZ331129 1M0056M21
C 54	15.2	40.0	50 1	AU105968 AU105968
C 55	15.2	40.0	61 1	AI1318033 t575902.x
C 56	15.2	40.0	66 3	AY432564 Aedes_aeg
C 57	15.2	40.0	76 8	BH011379 BG01292-5
C 58	15.2	40.0	79 8	AZ918914 1006013C0
C 59	15.2	40.0	81 8	AZ220216 1006018G0
C 60	15.2	40.0	82 1	AI973602 bC07B01.Y
C 61	15.2	40.0	84 8	AZ587706 1M0359L01
C 62	15.2	40.0	84 8	AZ918688 1006005F0
C 63	15.2	40.0	86 8	AZ918789 1006007G1
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C 65	15.2	40.0	92 8	BZ424945 100022272
C 66	15.2	40.0	92 9	AL952395 Arabidops
C 67	15.2	40.0	92 9	CG734095 1119162G0
C 68	15.2	40.0	95 9	CG617247 OST110506
C 69	15.2	40.0	96 1	AJ742933 AJ742933
C 70	15.2	40.0	99 2	BE133971 601504092
C 71	15	39.5	64 1	AI886867 wK29f04.x
C 72	15	39.5	76 6	CB260120 94-E9536-
C 73	15	39.5	76 7	CN850154 000917A0F
C 74	15	39.5	77 9	CG510398 OST62098
C 75	15	39.5	79 1	AI153240 uc51b07.r
C 76	15	39.5	81 1	AV858416 AV858416
C 77	15	39.5	88 4	BM114142 ACS62-DMS
C 78	15	39.5	89 9	CG537563 OST126682
C 79	15	39.5	95 9	AJ587756 Arabidops
C 80	15	39.5	96 2	BF137294 601781654
C 81	15	39.5	100 4	BJ263250 BJ263250
C 82	14.8	38.9	50 9	BX977848 Forward.B
C 83	14.8	38.9	52 2	AM696628 NF107B115
C 84	14.8	38.9	57 2	AM633542 b1096407.w
C 85	14.8	38.9	57 8	B02241 CSR1-150B11
C 86	14.8	38.9	63 6	CB070218 1627612.Y
C 87	14.8	38.9	63 9	CG653178 OST146535
C 88	14.8	38.9	68 9	CG546712 OST146535
C 89	14.8	38.9	73 4	BI094826 EST-CD34N
C 90	14.8	38.9	75 9	CG512276 OST65121
C 91	14.8	38.9	77 6	CD944539 RDK_19_Ge
C 92	14.8	38.9	77 6	CD965817 SEL_217_Ge
C 93	14.8	38.9	79 1	AA929672 vY75B09.r
C 94	14.8	38.9	80 9	CG658020 OST433475
C 95	14.8	38.9	83 9	CR137364 Reverse.B
C 96	14.8	38.9	87 1	AJ540137 AJS40137
C 97	14.8	38.9	87 4	BI546018 603188148

C 98 14.8 38.9 87 8 BH609273 2896 L1.8
 99 14.8 38.9 91 8 BH903262 1023
 C 100 14.8 38.9 92 6 CB395266 CB395266 OSTRI52G4

ALIGNMENTS

RESULT 1
 LOCUS A133954
 DEFINITION A133954 63 bp mRNA linear EST 17-DEC-1998
 u148c01.y1 Sugano mouse liver mlia mus musculus cDNA clone
 IMAGE:193264.5 similar to gb:X03524 Mouse mRNA for group 1 major
 urinary protein (MOUSE), mRNA sequence.

ACCESSION A133954.1 GI:4029080
 VERSION A133954
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 63)
 AUTHORS Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
 Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
 Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
 Waterston, R.
 TITLE The WashU-HMI Mouse EST Project
 JOURNAL Unpublished (1996)
 COMMENT Contact: Marra M/Mouse EST Project
 WashU-HMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810

EMAIL: mouseest@watson.wustl.edu
 This clone is available royalty-free through LML; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:979556
 Trace considered overall poor quality
 Seg primer: custom primer used
 High quality sequence stop: 1.
 Location/Qualifiers

FEATURES

source

1..63
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL"
 /db_xref="taxon:10090"
 /clone="IMAGE:193264"
 /sex="female"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="Sugano mouse liver mlia"
 /note="Organ: liver; Vector: pME18-F13; Site_1: DraIII
 (CACGCTGTG); Site_2: DraIII (CACGCTGTG); 1st strand cDNA
 was primed with an oligo(dT) primer
 [ATGAGGCGCTTTTCTTTTCTTTT]; double-stranded cDNA was
 ligated to a DraIII adaptor (TTTGGCTACTGTG), digested
 and cloned into distinct DraIII sites of the pME18-F13
 vector (5' site CACGCTGTG, 3' site CACGCTGTG). XhoI should
 be used to isolate the cDNA insert. Size selection was
 performed to exclude fragments <1.5kb. Library
 constructed by Dr. Sumio Sugano (University of Tokyo
 Institute of Medical Science). Custom primers for
 sequencing: 5' end primer CTTGCGCTCTAAAGCTGCG and 3' end
 primer CGACTGCACTCGACGACA."

ORIGIN

Query Match 46.3%; Score 17.6; DB 1; Length 63;
 Best Local Similarity 59.4%; Pred. No. 7.9e+03;
 Matches 19; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

1 CUCGCAUCUGAUGAGCGCGUUGAGCCGAA 32

Db 11
 CCTTCAGCTGATGGGTGTGTATGCGCCGAGAA 42

RESULT 2
 LOCUS A2368574 59 bp DNA linear GSS 02-OCT-2000
 DEFINITION 1M0118A16R Mouse 10kb plasmid UGCG1M library Mus musculus genomic
 clone UGCG1M0118A16 R, genomic survey sequence.

ACCESSION A2368574
 VERSION A2368574.1 GI:10482274
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 59)
 AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts

UNPUBLISHED (2000)
 CONTACT: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
 84112 USA
 TEL: 801 585 5606
 FAX: 801 585 7177

EMAIL: ddunn@genetics.utah.edu
 INSERT LENGTH: 10000 Std Error: 0.00
 PLATE: 0118 row: A column: 16
 SEQ PRIMER: CACACAGAAACAGCTATGACC
 CLASS: plasmid ends
 High quality sequence stop: 59.
 Location/Qualifiers

FEATURES

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 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCG1M0118A16"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UGCG1M library"
 /note="Vector: pMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD2 (gi|4732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

ORIGIN

Query Match 45.3%; Score 17.2; DB 8; Length 59;
 Best Local Similarity 53.3%; Pred. No. 1.2e+04;
 Matches 16; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

8 UCUGAUGAGCGCGUUGAGCCGAAAUUCAG 37

ACCESSION BH803188
 VERSION BH803188.1 GI:20318089
 KEYWORDS GSS.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 92)
 Walbot, V.
 Maize genomic sequences found using engineered RescueMu transposon
 Unpublished (2001)
 COMMENT Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Possible ligation site of ends cut by 2 different endonucleases.
 Reverse complemented post-ligation sequence from source sequence.
 Plate: 1008099 row: 14
 Class: transposon-tagged.
 Location/Qualifiers
 1..92
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 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_1ib="1008 - RescueMu Grid 1"
 /note="Organ: leaf; Vector: RescueMu (engineered from
 Bluescript backbone); Site 1: BamHI; Site 2: BglII;
 RescueMu is a 4.9 kb, modified maize Mu transposon
 designed to allow plasmid rescue from total genomic DNA.
 Mu elements insert preferentially into transcription
 units. For more information on RescueMu, go to the web
 site www.zmdb.lastate.edu and follow the links for
 'RescueMu.' Grid 1 was grown at Berkeley in 2001. DNA was
 extracted from leaf punches, double digested using BamHI
 and BglII, and ligated to form circular plasmids. DH10B
 cells were transformed and then screened on LB plates with
 ampicillin."

ORIGIN
 Query Match 44.7%; Score 17; DB 8; Length 92;
 Beet Local Similarity 57.6%; Pred. No. 1.5e+04;
 Matches 19; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 1 CCUGCAUUCGAGGCGCCGUAAGCGCGAATAA 33
 DB 57 CCTGCACATGATGAGTGTGTAGCGCTGAGAGA 89

RESULT 6
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 DEFINITION clone UUGC1M0070F19 F, genomic survey sequence.
 ACCESSION AZ807494
 VERSION AZ807494.1 GI:12971898
 KEYWORDS GSS.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 94)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenan, E., Pedersen, T.,
 Reilly, M., Rose, R., Rose, R., Stokes, R., Tingey, A., von
 Niederhausern, A. and Wright, D., Weiss, R.

REFERENCE
 AUTHORS

TITLE Mouse whole genome scaffolding with paired end reads from 10kb
 JOURNAL plasmid inserts
 COMMENT Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0070 row: F column: 19
 Seq primer: CGTGTAAACGACGCGCCAGT
 Class: plasmid ends
 High quality sequence stop: 94.
 Location/Qualifiers
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 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUGC2M0070F19"
 /sex="Male"
 /lab_host="B. Coli strain XL10-Gold, T1-resistant, F-"
 /clone_1ib="Mouse 10kb plasmid UUGC1M library"
 /note="Vector: PMD42nv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adaptor DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PMD42 (g14732114|gb|AF129072.1), a copy-number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

ORIGIN
 Query Match 44.7%; Score 17; DB 8; Length 94;
 Beet Local Similarity 57.6%; Pred. No. 1.5e+04;
 Matches 19; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 5 CAUUCGAGGCGCCGUAAGCGCGAATAAUCAG 37
 DB 88 CAGTGTATGAGCGCGAATGTCGCGCCATCAG 56

RESULT 7
 AU105965/c 50 bp mRNA linear EST 28-JAN-2004
 LOCUS AU105965
 DEFINITION HRC00826, mRNA sequence.
 ACCESSION AU105965
 VERSION AU105965.1 GI:1355486
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 50)
 Suzuki, Y., Taira, H., Tanoda, T., Mizushima-Sugano, J., Sese, J.,
 Hara, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
 Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
 Diverse transcriptional initiation revealed by fine, large-scale

REFERENCE
 AUTHORS

JOURNAL
EMBO Rep. 2 (5), 388-393 (2001)
MEDLINE
21270072
PUBMED
11375929
COMMENT
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ime.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
Sugano, S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

FEATURES
source
1..50
/organism="Homo sapiens"
/mol_type="mRNA"
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/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match 44.2%; Score 16.8; DB 1; Length 50;
Best Local Similarity 57.1%; Pred. No. 1.7e+04;
Matches 16; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

OY 2 CUGCAUCUGAGGCGGUGAGCCGA 29
DB 42 CTGCACATGACAGAGCCGTTGTCCGA 15

RESULT 8
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LOCUS AUI05967 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION HRC05018, mRNA sequence.
ACCESSION AUI05967
VERSION AUI05967.1 GI:13555488
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 50)
Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,
Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,
Sakaki, Y., Nakamura, Y., Suyama, A. and Sugano, S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
JOURNAL
MEDLINE
PUBMED
21270072
11375929
COMMENT
Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ime.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
Sugano, S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

FEATURES
source
1..50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match 44.2%; Score 16.8; DB 1; Length 50;
Best Local Similarity 57.1%; Pred. No. 1.7e+04;
Matches 16; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

OY 2 CUGCAUCUGAGGCGGUGAGCCGA 29
DB 34 CTGCACATGACAGAGCCGTTGTCCGA 7

RESULT 9
A1341480 55 bp mRNA linear EST 13-FEB-1999
LOCUS g994b11.x1 Soares total fetus Nb2HP8 9w Homo sapiens cDNA clone
DEFINITION IMAGE:1939005 3', similar to TR:Q15726 Q15726 MALIGNANT MELANOMA
METASTASIS-SUPPRESSOR, contains TARI.ct TARI repetitive element ;,
mRNA sequence.
ACCESSION A1341480
VERSION A1341480.1 GI:4078407
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 55)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: c9apbs-remail.nih.gov
This clone is available royalty-free through LML; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 527 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 1.
Location/Qualifiers
1..55
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="IMAGE:1939005"
/dev_stage="8-9 weeks"
/lab_host="DH10B"
/clone_lib="Soares total fetus Nb2HP8 9w"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; let strand cDNA
was prepared from mRNA obtained from pooled 8-9 week
(total) fetus material with a Not I - oligo(dT) primer [5'
TGTTCACATCTGAGGTGGAGCGCGCTTAATTTTATTTTT 3'].
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization, and was
constructed by Bento Soares and M. Patricia Bonaldo."

ORIGIN

Query Match 44.2%; Score 16.8; DB 1; Length 55;
Best Local Similarity 64.3%; Pred. No. 1.7e+04;
Matches 18; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

OY 7 AUCUGAGGCGGUGAGCCGCAAAAU 34
DB 5 ATCCGCTGAGGCCAAAGGCCACAAAT 32

RESULT 10
AV536751/c 91 bp mRNA linear EST 20-FEB-2004
LOCUS AV536751 Arabidopsis thaliana liquid-cultured seedlings Columbia
DEFINITION Arabidopsis thaliana cDNA clone pAZN10502R 5', mRNA sequence.
ACCESSION AV536751
VERSION AV536751.1 GI:8697034
KEYWORDS EST.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 91)

Asanizu,E., Nakamura,Y., Sato,S. and Tabata,S.
A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries
DNA Res. 7 (3), 175-180 (2000)

20363093
PUBMED
10907847

CONTACT: Erika Asanizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asanizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.

FEATURES
source
1..91
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/ecotype="Columbia"
/db_xref="taxon:3702"
/clone="PAZNI10502R"
/tissue_type="liquid-cultured seedlings"
/clone_lib="Arabidopsis thaliana liquid-cultured seedlings Columbia"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2: XhoI"

ORIGIN
Query Match 43.7%; Score 16.6; DB 1; Length 91;
Best Local Similarity 51.6%; Pred. No. 2.3e+04;
Matches 16; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 3 UGCAUUCGAGUAGCGCGUAGCGCAAAA 33
Db 91 TCGCAATTGTTTCACACGTTTAGGTGAAAA 61

RESULT 11
BX655236 67 bp DNA linear GSS 04-APR-2004
LOCUS Arabidopsis thaliana T-DNA flanking sequence GK-587H12-021350,
DEFINITION genomic survey sequence.
ACCESSION BX655236
VERSION BX655236.1 GI:37611624
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE
AUTHORS Li,Y., Rosso,M.G., Strizhov,N., Viehovever,P. and Weisshaar,B.
TITLE GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana
JOURNAL Bioinformatics 19 (11), 1441-1442 (2003)
MEDLINE 22755829
PUBMED 12874060

2 Rosso,M.G., Li,Y., Strizhov,N., Reiss,B., Dekker,K. and Weisshaar,B.
An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics
Plant Mol. Biol. 53 (1-2), 247-259 (2003)

JOURNAL 23117147
MEDLINE 14756321
PUBMED

3 Strizhov,N., Li,Y., Rosso,M.G., Viehovever,P., Dekker,K.A. and Weisshaar,B.
High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines

JOURNAL Biotechniques 35 (6), 1164-1168 (2003)
PUBMED 14682050
REFERENCE 4 (bases 1 to 67)
AUTHORS Li,Y., Strizhov,N., Rosso,M.G. and Weisshaar,B.
TITLE Direct Submission
JOURNAL Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer Zuechtungsforshung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
COMMENT This sequence has been recovered from the left border of the T-DNA. It indicates an insertion close to or within gene At1g55130. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: http://www.mpiz-koeln.mpg.de/GABI-Kat/.

FEATURES
source
1..67
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
/db_xref="taxon:3702"
/clone="GK-587H12-021350"
/ecotype="col-0"
/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pGABII (Genbank accession number: AY529716). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

ORIGIN
Query Match 43.2%; Score 16.4; DB 9; Length 67;
Best Local Similarity 58.8%; Pred. No. 2.7e+04;
Matches 20; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

QY 4 GCAUUCGAGUAGCGCGUAGCGCAAAUACAG 37
Db 14 GAAACGATTGAGCGCGTTAGACGAAAAACGAG 47

RESULT 12
CN165896 100 bp mRNA linear EST 02-APR-2004
LOCUS CN165896/c
DEFINITION 996741 MARC 4PIG Sus scrofa cDNA 3', mRNA sequence.
ACCESSION CN165896
VERSION CN165896.1 GI:46180326
KEYWORDS EST.
SOURCE Sus scrofa (pig)
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

REFERENCE
AUTHORS Smith,T.P.L., Freking,B.A., Ford,J.J., Vallet,J.L., Wise,T.A., Nonnenman,D.J., Wray,J.E. and Keele,J.W.
TITLE Porcine EST collection using a normalized library constructed from embryos representing early developmental stages
JOURNAL Unpublished (2003)
COMMENT Contact: Smith TP
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smitht@mail.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_alt option. Vector identified with cross_match v0.990329.
Plate: TMM8065 row: B column: 17
Seq primer: TAGAAGCAGCAGTCGACG.

FEATURES
source
1..100
/organism="Sus scrofa"

ORIGIN

/mol_type="mRNA"
/db_xref="taxon:9823"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_11b="MARC 4P1G"
/note="Vector: pCDNA3.1; Site_1: EcoRI; Site_2: NotI;
library made with combined RNA from day-10, day-13,
day-15, day-25, and day-30 whole embryos."

Query Match 43.2%; Score 16.4; DB 7; Length 100;
Best Local Similarity 58.8%; Pred. No. 2.8e+04;
Matches 20; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

5 CAUUCGAGGAGCGGUAAGCCGAAAUACAG 38
84 CAAAGTTCTGAGGACTGAGCGAGCAGAACAG 51

RESULT 13
LOCUS BH913847 90 bp DNA linear GSS 12-SEP-2002
DEFINITION 3526_1_41_1_C09.2EL_X_1 3526 - Rescuemu Grid K Zea mays genomic,
genomic survey sequence.
ACCESSION BH913847
VERSION BH913847.1 GI:22800392
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 90)
Malbot V.

REFERENCE
AUTHORS Maize genomic sequences found using engineered Rescuemu transposon
TITLE Unpublished (2001)
JOURNAL Contact: Malbot V
COMMENT Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu

Possible ligation site of ends cut by 2 different endonucleases.
Reverse complemented post-ligation sequence from source sequence.
Plate: 3526_1_41_1 row: 8
Classes: transposon-tagged.
Location/Qualifiers
1..90

FEATURES

source

/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_11b="3526 - Rescuemu Grid K"
/note="Organ: leaf; Vector: Rescuemu (engineered from
pBluescript backbone); Site_1: BamHI; Site_2: BglII;
Rescuemu is a 4.9 kb, modified maize mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on Rescuemu, go to the web
site "www.zmbl.iastate.edu" and follow the links for
"Rescuemu." Grid K was grown at Molokai, Hawaii in winter
2000-2001. DNA was extracted from leaf punches, double
digested using BamHI and BglII, and ligated to form
circular plasmids. DH10B cells were transformed and then
screened on LB plates with ampicillin."

ORIGIN

Query Match 42.6%; Score 16.2; DB 8; Length 90;
Best Local Similarity 62.1%; Pred. No. 3.4e+04;

Matches 18; Conservative 3; Mismatches 8; Indels 0; Gaps 0;
1 CCUGCAUUCGAGGCGGUAAGCCGAA 29
45 CCGGAGCTGAAGAGACGCTCGCCAA 73

RESULT 14
LOCUS CD971713 73 bp mRNA linear EST 16-JUL-2003
DEFINITION OAE12h01.y9 QAE Zea mays cDNA clone OAE12h01, mRNA sequence.
ACCESSION CD971713
VERSION CD971713.1 GI:32832035
KEYWORDS EST.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 73)
Genopiante.
Genopiante, a major partnership french program in plant genomes
Unpublished (2003)
Contact: Genopiante
Genopiante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomes programme 'Genopiante' (<http://www.genopiante.com>
and <http://genopiante-info.infobiogen.fr>).
Location/Qualifiers
1..73

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

FEATURES

source

/organism="Zea mays"
/mol_type="mRNA"
/cultivar="F2"
/db_xref="taxon:4577"
/clone="OAE12h01"
/tissue_type="pericarp"
/clone_11b="QAE"

ORIGIN

Query Match 42.1%; Score 16; DB 6; Length 73;
Best Local Similarity 62.5%; Pred. No. 4.1e+04;
Matches 20; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

1 CCUGCAUUCGAGGCGGUAAGCCGAA 32
8 CCTGAATACGAGGCTTGCCTTAAGCTGA 39

RESULT 15
LOCUS AJ597197 82 bp DNA linear GSS 15-JAN-2004
DEFINITION Arabidopsis thaliana T-DNA flanking sequence, left border, clone
447A09, genomic survey sequence.
ACCESSION AJ597197
VERSION AJ597197.1 GI:37946825
KEYWORDS GSS; left border; T-DNA flanking sequence.
SOURCE Arabidopsis thaliana (thale cress)

ORGANISM

Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eustosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE
AUTHORS Brunaud V., Balzergue S., Dubreucq B., Aubourg S., Samson F.,
Chavain S., Bechtold N., Cruaud C., DeRose R., Pelletier G.,
Leplancet L., Caboche M. and Lecharny A.

TITLE

T-DNA integration into the Arabidopsis genome depends on sequences
of pre-insertion sites
JOURNAL EMO Rep. 3 (12), 1152-1157 (2002)
MEDLINE 22363535
PUBMED 12446565

REFERENCE 2 (bases 1 to 82)
AUTHORS Balzerque, S.
TITLE Direct Submision
JOURNAL Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue
Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT PCR was performed on DNA from transformants of Arabidopsis thaliana
plants from INRA (Versailles). The DNA fragment(s) resulting from
the PCR were directly sequenced from the left or the right border
to determine the genomic sequence flanking the insertion. T-DNA
derived sequences were removed. Information to order the
corresponding mutant line and a link to a database providing a
graphical display of the insertion site are available at
http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
been generated in the framework of the French plant genomics
program 'Genoplante' (http://www.genoplante.com and
http://genoplante-info.infobiogen.fr).
Location/Qualifiers
1..82
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/cultivar="Massillewskija"
/db_xref="taxon:3702"
/clone="447A09"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
misc_feature
1..82 DNA flanking sequence
/note="T-DNA flanking sequence
left border"

Query Match 42.1%; Score 16; DB 9; Length 82;
Best Local Similarity 57.6%; Pred. No. 4.1e+04;
Matches 19; Conservative 3; Mismatches 11; Indels 0; Gaps 0;

Qy 6 AAUCGAGAGCGCCGUAAGCCGAAAUACAG 38
||:|||||
1 AATATGATTAGCCCTCAGACGAAAUAAACAG 33

Db 1 AATATGATTAGCCCTCAGACGAAAUAAACAG 33

RESULT 16
LOCUS BU029544 91 bp mRNA linear EST 26-SEP-2003
DEFINITION BU029544 NIBB Mochii normalized Xenopus neurola library Xenopus
laevis cDNA clone X1012m10 5', mRNA sequence.
ACCESSION BU029544
VERSION BU029544.1 GI:17369178
KEYWORDS EST.
SOURCE Xenopus laevis (African clawed frog)
ORGANISM Xenopus laevis
Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
Xenopodinae; Xenopus; Xenopus.
1 (bases 1 to 91)
Kitsayama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-I, T. and
Kohara, Y.
Expressed genes in X. laevis embryo
Unpublished (2001)
Contact: Tadaeu Shin-I
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp
The information of this clone is available through the following
URL.
http://xenopus.nibb.ac.jp.
Location/Qualifiers
1..91
/organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="X1012m10"
/tissue_type="whole embryo"

FEATURES
source

ORIGIN /dev_stage="stage 15"
/clone_lib="NIBB Mochii normalized Xenopus neurola
library"

Query Match 42.1%; Score 16; DB 4; Length 91;
Best Local Similarity 70.8%; Pred. No. 4.2e+04;
Matches 17; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 8 UCUGAGAGCGCCGUAAGCCGAA 31
:|||||
15 TCTGAAGAGCCGACGCTGAA 38

Db 15 TCTGAAGAGCCGACGCTGAA 38

RESULT 17
LOCUS AI204769 94 bp mRNA linear EST 14-OCT-1998
DEFINITION ZF-EST88 Zebrafish cDNA library Danio rerio cDNA clone M88 3',
mRNA sequence.
ACCESSION AI204769
VERSION AI204769.1 GI:3757375
KEYWORDS EST.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 94)
Huh, T.L., Park, H.C., Yeo, S.Y., Hong, S.K. and Kim, S.H.
Rapid identification and isolation of zebrafish cDNA clones
(Huh, T.L. et al.)
Unpublished (1998)
Contact: Tae-Iin, Huh
Department of Genetic Engineering
College of Natural Sciences, Kyungpook National University
1370 Bankyuk-dong, Pukku, Taegu 702-701, S. Korea
Tel: +82 53 950 5387
Fax: +82 53 943 9755
Email: tlnh@kyungpook.ac.kr
Insert Length: 94 Std Error: 0.00
Seq primer: T7 promoter primer
High quality sequence atp: 93.
Location/Qualifiers
1..94
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/clone="M88"
/sex="male and female mix"
/tissue_type="embryonic"
/dev_stage="6 - 48 hours post fertilization"
/clone_lib="Zebrafish cDNA library"

FEATURES
source

Query Match 42.1%; Score 16; DB 1; Length 94;
Best Local Similarity 53.1%; Pred. No. 4.2e+04;
Matches 17; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

Qy 6 AAUCGAGAGCGCCGUAAGCCGAAAUACAG 37
||:|||||
34 AATCGATGATGTCTTCGACAGATCTCG 65

Db 34 AATCGATGATGTCTTCGACAGATCTCG 65

RESULT 18
LOCUS AA237314 97 bp mRNA linear EST 03-MAR-1997
DEFINITION wx17b12.r1 Soares mouse NMU Mus musculus cDNA clone IMAGE:660447 5',
similar to TR:G1136414 G1136414 KIAA0177 PROTEIN ;, mRNA sequence.
ACCESSION AA237314
VERSION AA237314.1 GI:1861335
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

TITLE Construction of long-transcript enriched cDNA libraries from submicrogram amounts of total RNAs by a universal PCR amplification method

JOURNAL MEDLINE PUBMED Genome Res. 11 (9), 1553-1558 (2001) 21429098 11544199

COMMENT Contact: George J. Kargul
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@jgun.grc.nia.nih.gov
nlaest: http://jgun.grc.nia.nih.gov/cdna/cdna.html
nlaest: L0955 row: G column: 10
Seq primer: -21M13 Reverse
High quality sequence stop: 89
POLYA=No.

FEATURES Location/Qualifiers

source 1..89

/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="nlaest:L0955G10-5"
/db_xref="taxon:10090"
/clone="L0955G10"
/cissue_type="Newborn Kidney"
/dev_stage="Newborn"
/lab_host="DHI08"
/clone_1lb="NIA Mouse Newborn Kidney cDNA Library2 (short)"
/note="Vector: pSPORT1 (Invitrogen); Site 1: SalI; Site 2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://jgun.grc.nia.nih.gov/cdna). This is a short-transcript enriched cDNA library (Ref. Genome Res. 11:1553-1558 (2001). [PMID: 11544199]). In brief, double-stranded cDNAs were synthesized with an Oligo(dT) primer (Invitrogen: 5'-PACATGATCTGATCGCAGCGCCGCTTTT-3') from 26 ug of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to lone-linker L1-salI, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-L. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pSPORT1 plasmid vector. The DHI08 E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 1.5 kb. The library was constructed by Yulan Plao (NIA)."

ORIGIN

Query Match 41.6%; Score 15.8; DB 4; Length 89;
Best Local Similarity 63.0%; Pred. No. 5.1e+04;
Matches 17; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 11 GAUGAGGCGGUAAGCCGAAAUAUCAG 37
||:|||||:|||||:|||||
Db 67 GATGGGGCTGTAGGCCAATGAATGAG 41

RESULT 24 CG663893 92 bp mRNA linear GSS 02-OCT-2003
LOCUS CG663893
DEFINITION OST450022 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST450022, mRNA sequence.
ACCESSION CG663893
VERSION CG663893.1 GI:37487742
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 92)

AUTHORS Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J., Piggett, J., BeltrandelRio, H., Buxton, E.C., Edwards, J., Finch, R.A., Fiddie, C.J., Gupta, A., Hansen, G., Hu, Y., Huang, W., Jiang, C., Key, B.W., Jr., Kipp, P., Kohlhauff, B., Ma, Z.-Q., Marlesch, D., Payne, R., Potter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z., Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N., Zhu, Q., Person, C. and Sande, A.T.
Mki kinase deficiency lowers blood pressure in mice: a gene-trap screen to identify potential targets for therapeutic intervention Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
Contact: Zambrowicz BP
OmniBank
Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: materials@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as described in Zambrowicz et al (Nature. 1998 Apr 9;392(6676):608-11)
Class: Gene trap.

FEATURES Location/Qualifiers

source 1..92

/organism="Mus musculus"
/mol_type="mRNA"
/strain="129Sv/Ev"
/db_xref="taxon:10090"
/clone="OST450022"
/cell_type="embryonic stem cell"
/clone_1lb="Mus musculus 129Sv/Ev"

ORIGIN

Query Match 41.6%; Score 15.8; DB 9; Length 92;
Best Local Similarity 50.0%; Pred. No. 5.2e+04;
Matches 18; Conservative 5; Mismatches 13; Indels 0; Gaps 0;

QY 1 CCUGCAUUCGUAUGAGCCGUAAGCCGAAAUAUCA 36
||:|||||:|||||:|||||
Db 44 CCTGCAACTCCTCAGCCCGTAGCTTACAGATCA 9

RESULT 25 CD947628 94 bp mRNA linear EST 15-JUL-2003
LOCUS SAA.70 GeneTag2 Zea mays cDNA, mRNA sequence.
DEFINITION CD947628
ACCESSION CD947628.1 GI:32795392
KEYWORDS EST.
SOURCE Zea mays
Zea mays
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD clade; Panicoidae; Andropogoneae; Zea.
1 (bases 1 to 94)

REFERENCE Genoplane.
Genoplane, a major partnership french program in plant genomics Unpublished (2003)
Contact: Genoplane

QY 93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french plant genomics programme 'Genoplane' (http://www.genoplane.com and http://genoplane-info.infobiogen.fr).

FEATURES Location/Qualifiers

source 1..94

/organism="Zea mays"
/mol_type="mRNA"
/cultivar="mixture"
/db_xref="taxon:4577"
/clone_1lb="GeneTag2"

ORIGIN

```
/organism="Mus musculus"  
/mol_type="genomic DNA"  
/strain="C57BL/6J"
```


from contaminating host leukocytes by filtration of ADP activated blood through acid-washed glass beads and Matman Cfil cellulose columns by gravity filtration. Purified DNA was digested with mung bean nuclease in the presence of 42.5% formamide at 500C as described (Gallinski, M. et al. 1992. Cell 69,1213-1226; Vernick, K.D. et al.1988. N.A.R. 16, 6883-6896). Eco RI linkers were added and the constructs ligated into Lambda ZAP II. P. vivax Belem was originally isolated from a patient in Belem, Brazil 1980 by Mercia de Arruda, adapted to Saimiri monkeys by Jurg Gysin, and maintained since 1983 in squirrel monkeys."

ORIGIN

Query Match 41.6%; Score 15.8; DB 8; Length 98;

Best Local Similarity 54.3%; Pred. No. 5.2e+04;
Matches 19; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

Qy 2 CUGCAUUCGUAUGGCCGCUUAGCCGAAAUCA 36
18 CTGCAAAAGGCTTATTCAGTTAGAGAAAGGCA 52

RESULT 31
AJ590916 41 bp DNA linear GSS 15-JAN-2004
LOCUS Arabidopsis thaliana T-DNA flanking sequence, left border, clone
DEFINITION 576H02, genomic survey sequence.
ACCESSION AJ590916
VERSION AJ590916.1 GI:37940540
KEYWORDS GSS; left border; T-DNA flanking sequence.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eustosids II; Brassicales; Brassicaceae; Arabidopsids.

REFERENCE

AUTHORS

1 Brunaud, V., Balzerque, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G., Lepoint, L., Caboche, M. and Lecharny, A.
T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites
EMBO Rep. 3 (12), 1152-1157 (2002)

JOURNAL

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

2 (bases 1 to 41)
Balzerque, S.
Direct Submission
Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE
PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbsgap.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomics program 'genoplante' (<http://www.genoplante.com> and <http://genoplante-info.infobiogen.fr>).
Location/Qualifiers
1..41
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/culivar="Wassiljewskij3a"
/db_xref="taxon:3702"
/clone="576H02"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
1..41
/note="T-DNA flanking sequence
left border"

FEATURES

SOURCE

ORIGIN

misc_feature

left border"

Query Match 41.1%; Score 15.6; DB 9; Length 41;
Best Local Similarity 52.6%; Pred. No. 5.6e+04;
Matches 20; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

Qy 1 CCUGCAUUCGUAUGGCCGCUUAGCCGAAAUCAAGC 38
2 CCAAAAGCTGACGAAGACGTTACGACGAGAGAGAGG 39

RESULT 32

LOCUS

AI702572 76 bp mRNA linear EST 18-DEC-1999
DEFINITION we80b03.x1 Soares NPL T GBC S1 Homo sapiens cDNA clone
IMAGE:2347373 3', mRNA sequence.
ACCESSION AI702572
VERSION AI702572.1 GI:4990472
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 76)
NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
This clone is available royalty-free through LNL; contact the IMAGE Consortium (infoimage.llnl.gov) for further information.
Insert Length: 544 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 65.
Location/Qualifiers
1..76
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2347373"
/lab_host="BDH10B"
/clone_lib="Soares_NPL_T_GBC_S1"
/note="Organ: pooled; Vector: pTT3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not 1; Site 2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NBH19W, testis NHT, and B-cell NCI CGAP GCB1) were mixed and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Patricia Bonaldi."

FEATURES

SOURCE

ORIGIN

misc_feature

left border"

ORIGIN

Query Match 41.1%; Score 15.6; DB 1; Length 76;
Best Local Similarity 68.2%; Pred. No. 6.1e+04;
Matches 15; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 11 GAUGAGCGCGUAGCCGCGAANA 32
13 GATGGGCTTTTACGCGCGAANA 34

RESULT 33

LOCUS

W72704 76 bp mRNA linear EST 17-OCT-1996
DEFINITION z671c05.61 Soares fetal heart NBH19W Homo sapiens cDNA clone
IMAGE:346088 3' similar to PIR:A26882 A26882 PIR2 hypothetical protein - rat; mRNA sequence.
W72704
W72704.1 GI:1382701

ACCESSION W72704
VERSION W72704.1 GI:1382701

KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Autors Butharia; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 76)
Hiller, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Maier, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevastis, E., Waterston, R., Williamson, A., Wohlmann, P., and
Wilson, R.
TITLE The Marsh-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Insert Length: 1248 Sca Error: 0.00
Seq primer: mob.REGA+ET
High quality sequence stop: 1.
Location/Qualifiers
1..76
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:1271463"
/db_xref="taxon:9606"
/clone="IMAGE:346088"
/sex="unknown"
/dev_stage="19 weeks"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares fetal heart NBHL19W"
/note="Organ: heart; Vector: pT73D (Pharmacia) with a
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
strand cDNA was primed with a Not I - oligo(dT) primer [5'
TTTTCACATCTGAGATGGAGCGCGCATCTTTTCTTTTCTTTT 3']
double-stranded cDNA was size selected, ligated to Eco RI
adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library went through one round of
normalization to a Cot = 5. Library constructed by
M. Fatima Bonaldo. This library was constructed from the
same fetuses as the fetal lung library, Soares fetal lung
NBHL19W."

ORIGIN
Query Match 41.1%; Score 15.6; DB 7; Length 76;
Best Local Similarity 52.6%; Pred. No. 6.1e+04;
Matches 20; Conservative 4; Mismatches 14; Indels 0; Gaps 0;

QY 1 CCUGCAUUCGAGGAGCGCGUAGCGCGAAGAAUACAG 38
DB 23 CTTCAATCAAGAGCTCCGCTGAGCTTGAATGAGG 60

RESULT 34
CG547582/c
LOCUS 78 bp mRNA linear GSS 01-OCT-2003
DEFINITION OST148394 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST148394,
mRNA sequence.
ACCESSION CG547582
VERSION CG547582.1 GI:37334169
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Butharia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 78)
Location/Qualifiers
1..80
/organism="Mus musculus"
/mol_type="mRNA"

AUTHORS Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J.,
Piggott, J., Beltrande-Rio, H., Buxton, E.C., Edwards, J., Finch, R.A.,
Fridde, C.J., Gupta, A., Hansen, G., Hu, Y., Hang, W., Jang, C.,
Key, B.W., Jr., Kipp, P., Kohlhaut, B., Ma, Z.-O., Markesich, D.,
Payne, R., Porter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z.,
Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N.,
Zhu, Q., Person, C., and Sands, A.T.
TITLE Wnt1 kinase deficiency lowers blood pressure in mice: a gene-trap
screen to identify potential targets for therapeutic intervention
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
COMMENT Contact: Zambrowicz BP
OmitBank
Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: material@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as
described in Zambrowicz et al (Nature, 1998 Apr 9;392(6676):608-11)
Class: Gene Trap.
Location/Qualifiers
1..78
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129Sv/Ev"
/db_xref="taxon:10090"
/clone="OST148394"
/cell_type="embryonic stem cell"
/clone_lib="Mus musculus 129Sv/Ev"

ORIGIN
Query Match 41.1%; Score 15.6; DB 9; Length 76;
Best Local Similarity 50.0%; Pred. No. 6.2e+04;
Matches 19; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

QY 1 CCUGCAUUCGAGGAGCGCGUAGCGCGAAGAAUACAG 38
DB 39 CCGTCTCTGGAGGAGATCTGAAGCGCAACCTTAGG 2

RESULT 35
CG545569
LOCUS 80 bp mRNA linear GSS 01-OCT-2003
DEFINITION OST143941 Mus musculus 129Sv/Ev Mus musculus cDNA clone OST143941,
mRNA sequence.
ACCESSION CG545569
VERSION CG545569.1 GI:37332156
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Butharia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 80)
Zambrowicz, B.P., Abuin, A., Ramirez-Solis, R., Richter, L.J.,
Piggott, J., Beltrande-Rio, H., Buxton, E.C., Edwards, J., Finch, R.A.,
Fridde, C.J., Gupta, A., Hansen, G., Hu, Y., Hang, W., Jang, C.,
Key, B.W., Jr., Kipp, P., Kohlhaut, B., Ma, Z.-O., Markesich, D.,
Payne, R., Porter, D.G., Qian, N., Shaw, J., Schrick, J., Shi, Z.-Z.,
Sparks, M.J., Van Sligtenhorst, I., Vogel, P., Walke, W., Xu, N.,
Zhu, Q., Person, C., and Sands, A.T.
TITLE Wnt1 kinase deficiency lowers blood pressure in mice: a gene-trap
screen to identify potential targets for therapeutic intervention
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 100 (24), 14109-14114 (2003)
COMMENT Contact: Zambrowicz BP
OmitBank
Lexicon Genetics Incorporated
4000 Research Forest Drive, The Woodlands, TX 77381, USA
Email: material@lexgen.com
Gene trap sequence tag generated by 3' RACE from mouse ES cells as
described in Zambrowicz et al (Nature, 1998 Apr 9;392(6676):608-11)
Class: Gene Trap.
Location/Qualifiers
1..80
/organism="Mus musculus"
/mol_type="mRNA"

VERSION BG881971.1 GI:14259063
 KEYWORDS EST.
 SOURCE Glycine max (soybean)
 ORGANISM Glycine max
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eustosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
 Glycine.
 1 (bases 1 to 99)
 Shoemaker R., Kelm P., Vodkin L., Erpelting J., Corryell V.,
 Khanna A., Bolla B., Marra M., Hillier L., Kucaba T., Martin J.,
 Beck C., Wylie T., Underwood K., Steptoe M., Theising B., Allen M.,
 Bowers Y., Person B., Swaller T., Gibbons M., Page D., Harvey N.,
 Schurk R., Ritter E., Kohn S., Shin T., Jackson Y., Cardenas M.,
 McCann R., Waterston R. and Wilson R.
 Contact: Shoemaker R./Public Soybean EST Project
 Public Soybean EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: eschwatson.wustl.edu
 When it has been determined, an EST from the other end of this
 clone is listed in the 'Other ESTs on clone' field. This clone is
 available through: Biogenetic Services, 801 32nd Ave. Brookings, SD
 57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)
 Insert Length: 1306 Std Error: 0.00
 High quality sequence stop: 99.
 Location/Qualifiers
 1..99
 /organism="Glycine max"
 /mol_type="mRNA"
 /cultivar="Williams"
 /db_xref="taxon:3847"
 /clone="GENOME SYSTEMS CLONE ID: Gm-c1065-3196"
 /tissue_type="germinating shoots"
 /lab_host="DH10B"
 /clone_1fb="Gm-c1065"
 /note="Vector: Bluescript II SK+, Site 1: EcoRI, Site 2:
 XhoI; The cDNA library was constructed from mRNA isolated
 germinating shoots of the cultivar Williams. The seeds
 were allowed to germinate for 24 hours prior to being
 cold stressed for 2 days at 4C. Complementary DNA was
 synthesized from mRNA using a primer consisting of a
 poly(dT) sequence with a XhoI restriction site. EcoRI
 adapters were ligated to the blunt-ended cDNA fragments
 followed by XhoI digestion. The cDNA fragments were
 directionally cloned into the EcoRI-XhoI restriction site
 of the Bluescript vector. The ligated cDNA fragments were
 transformed into DH10B host cells (GibcoBRL). This library
 was constructed in the laboratory of Dr. Randy
 Shoemaker."

ORIGIN
 Query Match 41.1%; Score 15.6; DB 4; Length 99;
 Best Local Similarity 52.6%; Pred. No. 6.4e+04;
 Matches 20; Conservative 4; Mismatches 14; Indels 0; Gaps 0;

QY 1 CCUGCAUUCGAGCGCGUAGCCGGAANAUCAGG 38
 Db 51 CTTCAATCTGGTGGAGCCCTCAAGGCTACAGATG 14

RESULT 39
 LOCUS CV316867 100 bp mRNA linear EST 24-SEP-2004
 DEFINITION CM2-BN0185-220400-166-ho2 BN0185 Homo sapiens cDNA, mRNA sequence.
 ACCESSION CV316867
 VERSION CV316867.1 GI:52640081
 KEYWORDS EST.
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 100)
 Dias Neto E., Garcia Correa R., Verjowski-Almeida S., Briones M.R.,
 Nagai M.A., da Silva M. Jr., Zago M.A., Bordin S., Costa F.F.,
 Goldman G.H., Carvalho A.F., Matsukuma A., Bala G.S., Simpson D.H.,
 Brunstein A., de Oliveira P.S., Bucher P., Jongeneel C.V.,
 O'Hare M.J., Soares F., Brentani R.R., Reis L.F., de Souza S.J. and
 Simpson A.J.
 Shotgun sequencing of the human transcriptome with ORF expressed
 sequence tags
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
 20202663
 MEDLINE 10737800
 PUBMED
 CONTACT: Simpson A.J.G.
 Laboratory of Cancer Genetics
 Ludwig Institute for Cancer Research
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
 Brazil
 Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome
 Project. <http://www.ludwig.org.br>.
 Location/Qualifiers
 1..100
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /dev_stage="Adult"
 /clone_1fb="BN0185"
 /note="Organ: breast normal; Vector: puc18; Site 1: SmaI;
 Site 2: SmaI; A mini-library was made by cloning products
 derived from ORESTES PCR (U.S. Letters Patent application
 No. 196,716 - Ludwig Institute for Cancer Research)
 profiles into the pUC 18 vector. Reverse transcription of
 tissue mRNA and cDNA amplification were performed under
 low stringency conditions."

ORIGIN
 Query Match 41.1%; Score 15.6; DB 7; Length 100;
 Best Local Similarity 53.3%; Pred. No. 6.4e+04;
 Matches 16; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

QY 9 CUGAGAGCGCGUAGCCGGAANAUCAGG 38
 Db 52 CTGTGAGCGCGTCTGGCGATCGATCTGG 23

RESULT 40
 LOCUS CC483070 51 bp DNA linear GSS 16-JUN-2003
 DEFINITION CH240_311111.TARAC13P2 CHORI-240 Bos taurus genomic clone
 CC483070
 ACCESSION CC483070
 VERSION CC483070.1 GI:31764069
 KEYWORDS GSS.
 SOURCE Bos taurus (cow)
 ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovinae; Bos.
 1 (bases 1 to 51)
 Holt R., Scott J., Yang G., Barber S., Smailus D., Prabh A.-L.,
 Tsai M., Cloutier A., Lee D., Giron N., Olson T., Mayo M.,
 Butterfield Y., Kirpatrick R., Liu J., Guin R., Chan A.,
 Mathewson C., Wye N., Masson A., Brown-John M., Jones S.,
 Schein J., Marra M., de Jong P., McWilliam S., Bartis W.,
 Dalrymple B.P. and Tellam R.
 Bovine BAC End Sequences from Library CHORI-240, PLATES 294 to 398
 Unpublished (2003)
 COMMENT Other_GSSs: CH240_311111.T7

Contact: Rob Holt
Sequencing
The British Columbia Cancer Agency Genome Science Centre
600 W. 10th Ave, Vancouver, British Columbia, Canada V5Z 4E6
Tel: 604-877-6085
Fax: 604-877-6276
Email: rholt@bcgsc.ca

Clones are derived from the bovine BAC library CHORI-240 (<http://www.chori.org/bacpac/bovine240.htm>). For BAC library availability, please contact Pieter de Jong (pdejongemail.cio.org). Clones may be purchased from BACPAC Resources (<http://www.chori.org/bacpac/orderinginformation.htm>). This work was undertaken as part of the International Bovine BAC Mapping Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the British Columbia Genome Sciences Centre, Canada.

Plate: 311 row: L column: 11

Seq primer: SP6

Class: BAC ends.

FEATURES

```

FEATURES
source
location/Qualifiers
1..51
/organism="Bos taurus"
/mol_type="genomic DNA"
/strain="Breed: Hereford"
/db_xref="taxon:9913"
/clone="CH240_311111"
/sex="Male"
/cell_type="Blood"
/clone_1lb="CHORI-240"
/note="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI,
Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC
library (Male) produced by Fiechter de Jong"

```

ORIGIN

Query Match	40.5%	Score 15.4	DB 9	Length 51
Best Local Similarity	60.0%	Pred. No. 7.1e+04		
Matches	15	Conservative	4	Mismatches 6
				Indels 0
				Gaps 0
QY	5	CAACUCGATGAGGCCGCUUAGGCCCA	29	
Db	26	CGACCTGATGAGGTGTGGGACCA	50	

Search completed: May 13, 2005, 17:51:09
Job time : 1864.87 secs